

proteoglycan, used for, e.g. obtaining compounds for  
reducing **atherosclerosis**.

DERWENT CLASS: B04 D16 S03  
INVENTOR(S): BOREN, J O S; INNERARITY, T L; BOREN, J; INNERARITY, T  
PATENT ASSIGNEE(S): (REGC) UNIV CALIFORNIA; (BORE-I) BOREN J; (INNE-I)  
INNERARITY T  
COUNTRY COUNT: 85  
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9946598	A1	19990916	(199946)*	EN	69
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL					
OA PT SD SE SL SZ UG ZW					
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD					
GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV					
MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT					
UA UG UZ VN YU ZW					
AU 9929842	A	19990927	(200006)		
EP 1062512	A1	20001227	(200102)	EN	
R: AT BE CH DE FR GB IE IT LI NL					
US 2001024797	A1	20010927	(200159)		
US 2001029027	A1	20011011	(200162)		
AU 760794	B	20030522	(200338)		
US 6579682	B1	20030617	(200341)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9946598	A1	WO 1999-US4805	19990305
AU 9929842	A	AU 1999-29842	19990305
EP 1062512	A1	EP 1999-911123	19990305
		WO 1999-US4805	19990305
US 2001024797	A1 Provisional	US 1998-77618P	19980310
	Div ex	US 1999-265222	19990305
		US 2001-823418	20010329
US 2001029027	A1 Provisional	US 1998-77618P	19980310
	Div ex	US 1999-265222	19990305
		US 2001-822965	20010329
AU 760794	B	AU 1999-29842	19990305
US 6579682	B1 Provisional	US 1998-77618P	19980310
		US 1999-265222	19990305

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9929842	A Based on	WO 9946598
EP 1062512	A1 Based on	WO 9946598
AU 760794	B Previous Publ.	AU 9929842
	Based on	WO 9946598

PRIORITY APPLN. INFO: US 1998-77618P 19980310; US 1999-265222  
19990305; US 2001-823418 20010329; US  
2001-822965 20010329

AB WO 9946598 A UPAB: 19991110

DETAILED DESCRIPTION - A novel method for identifying compounds that affect a **low density** lipoprotein (**LDL**) - proteoglycan (**PG**) binding comprises:

- (a) incubating a mixture by:
- (i) **PG**;
  - (ii) **LDL**, and
  - (iii) a candidate compound, where **LDL** binds to **PG** to form an **LDL-PG** complex in the absence of the candidate compound, and
- (b) determining any difference between the amount of **LDL-PG** complex present in:
- (i) the mixture as prepared in (a), and
  - (ii) an assay mixture comprising the **PG** and the **LDL** in the absence of the candidate compound.

INDEPENDENT CLAIMS are also included for the following:

- (1) an apo-B100 protein comprising a **PG** receptor mutation in Site B;
- (2) an **LDL** particle comprising an apo-B100 protein as in (1);
- (3) an antibody composition which binds to an antigenic determinant in an apo-B100 protein as in (1), where the antigenic determinant is not present in the wild-type human apo-B100 protein;
- (4) a polynucleotide (**PN**) encoding an apo-B100 protein as in (1), and
- (5) a cell comprising a **PN** as in (4), and
- (6) a non-human animal comprising a **PN** as in (4).

USE - The method can be used for identifying compounds which disrupt **LDL-PG** binding without inhibiting **LDL** receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or **LDL-PG** binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The **PNs** can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal.

ADVANTAGE - None given.

Dwg. 0/6

L91 ANSWER 40 OF 42 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN  
ACCESSION NUMBER: 1999-602336 [52] WPIDS  
DOC. NO. CPI: C1999-175415  
TITLE: New phosphorylated forms of sterol regulatory element  
**binding proteins** useful for treating or  
preventing **arteriosclerosis**, stroke and  
diabetes mellitus.  
DERWENT CLASS: B04 D16  
INVENTOR(S): KRONE, W; MUELLER-WIELAND, D  
PATENT ASSIGNEE(S): (KRON-I) KRONE W; (MUEL-I) MUELLER-WIELAND D  
COUNTRY COUNT: 87  
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
DE 19816902	A1	19991028	(199952)*		26
WO 9954352	A2	19991028	(199953)	GE	
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MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT  
 UA UG US UZ VN YU ZA ZW  
 AU 9943580 A 19991108 (200014)  
 EP 1071713 A2 20010131 (200108) GE  
 R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
DE 19816902	A1	DE 1998-19816902	19980416
WO 9954352	A2	WO 1999-DE1137	19990415
AU 9943580	A	AU 1999-43580	19990415
EP 1071713	A2	EP 1999-926248	19990415
		WO 1999-DE1137	19990415

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9943580	A Based on	WO 9954352
EP 1071713	A2 Based on	WO 9954352

PRIORITY APPLN. INFO: DE 1998-19816902 19980416

AB DE 19816902 A UPAB: 19991210

NOVELTY - Phosphorylated polypeptides, SREBP1 (sterol regulatory element binding proteins) (I) and SREBP2 (II), comprising 1146 and 1141 amino acid sequences, respectively, both fully defined in the specification and their allelic variants or derivatives with transcription factor activity, are new.

ACTIVITY - Anti-arteriosclerosis; cerebroprotective; cardiant; antidiabetic; antihypertensive; anorectic; nootropic; neuroprotective; hepatotrophic; antineurodegeneration.

MECHANISM OF ACTION - **Low density** lipoprotein (LDL) receptor stimulator, by binding to the sterol-regulatory cis-element in the LDL gene promoter, in a cholesterol-independent manner. The activity of (I) and (II) is regulated not only by the cholesterol content of cells but also by post-translational modification (phosphorylation).

USE - (I) and (II) are used to prevent or treat arteriosclerosis, stroke, coronary heart disease, peripheral arterial occlusive disease, glucose intolerance, diabetes mellitus, arterial hypertension, adiposity, disorders of fat metabolism, genetic hypertriglyceridemia (associated with lack of ApoC2), Alzheimer's disease, neurodegeneration and genetic liver disease which are modulated by SREBP responsive genes.

ADVANTAGE - Phosphorylation significantly increases transcriptional activity of SREBP-1 or -2.

Dwg.0/5

L91 ANSWER 41 OF 42 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

ACCESSION NUMBER: 1996-039954 [04] WPIDS

DOC. NO. CPI: C1996-013405

TITLE: Compsn. containing oligosaccharide(s) that **bind** to **lipoprotein** lipase - to prevent its interaction with receptors that would cause cellular uptake of lipoprotein, especially to treat or prevent **atherosclerosis**.

COUNTRY COUNT: 64  
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9533468	A1	19951214	(199604)*	EN	32
RW: AT BE CH DE DK ES FR GB GR IE IT KE LU MC MW NL OA PT SD SE SZ UG					
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LT LV MD MG MN MW MX NO NZ PL RO RU SD SG SI SK TJ TM TT UA UG US					
UZ VN					
AU 9525609	A	19960104	(199613)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9533468	A1	WO 1995-DK217	19950602
AU 9525609	A	AU 1995-25609	19950602

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9525609	A Based on	WO 9533468

PRIORITY APPLN. INFO: DK 1994-637 19940606  
AB WO 9533468 A UPAB: 19960129

Compsn. comprises, apart from carrier or diluent, an oligosaccharide of formula (I): dUAp2S(1=>4)-[alpha-DGlcNp2R16R2(1=>4)-X(1=>4)]n-alpha-D-GlcNp2R16R2, where dUAp2S = 4-deoxy-alpha-L-threo-hex-4-eno-pyranosyl-uronic acid, 2-sulphate; alpha-D-GlcNp = alpha-D-2-deoxy-2-amino-glucopyranose; X= Idoap2R2(alpha-L-ido-pyranosyl-uronic acid) or beta-D-GlcAp (beta-D-glucopyranosyl-uronic acid); R1=H, sulphate or acetyl; R2= H or sulphate, and n is an integer of 3-16. (I) can bind to lipoprotein lipase (LPL) to inhibit interaction between the alpha2-macroglobulin receptor/low density lipoprotein receptor-related protein (alpha2-MR/LRP) and LPL (or its complex with lipoprotein). Such as interaction would result in uptake of lipoprotein by mammalian cells.

USE - (I) are used to treat or prevent diseases involving interaction between alpha2-MR/LRP (especially when expressed on smooth muscle cells or macrophages) and LPL (or its complex with lipoprotein), specifically atherosclerosis. (I) is administered at 1-100 mg/kg, given by injection, orally, nasally or rectally.

ADVANTAGE - (I) lock the anticoagulant activity of heparin.

Dwg.0/3

L91 ANSWER 42 OF 42 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN  
ACCESSION NUMBER: 1991-353525 [48] WPIDS  
CROSS REFERENCE: 1989-356359 [48]; 1998-192802 [17]; 1999-539543 [45];  
1999-632641 [52]  
DOC. NO. CPI: C1991-152440  
TITLE: Synthetic peptide(s) comprising amphiphilic domain of apoA-I - used to diagnose vascular injury or disease or inhibit binding of low density lipoprotein to vascular walls in treating atherosclerosis.

PATENT ASSIGNEE(S): (NEWE-N) NEW ENGLAND DEACONESS HOSPITAL  
COUNTRY COUNT: 16  
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9116919	A	19911114	(199148)*		70
RW: AT BE CH DE DK ES FR GB GR IT LU NL SE					
W: AU CA JP					

PRIORITY APPLN. INFO: US 1990-518215 19900503; US 1990-518142  
19900503

AB WO 9116919 A UPAB: 19991221

Peptides and their analogues which comprise the following amino acid sequences are new.

Tyr-Lys-Leu-Ala-Leu -Glu-Ala-Ala-Arg-Leu-Leu-Ala -Asp-Ala-Glu-Gly-Ala-Lys; Tyr-Lys-Leu-Ala-Glu-Ala -Ala-Arg-Leu-Leu-Ala-Asn-Ala -Glu-Gly-Ala-Lys; Tyr-Arg-Ala-Leu-Val-Asp -Tyr-Leu-Lys-Phe-Val-Thr-Gln-Leu; Tyr-Arg-Ala-Leu -Val-Asp-Thr-Leu-Lys; Tyr-Ala-Lys-Phe-Arg-Glu-Thr -Leu-Glu-Asp-Thr-Arg-Asp-Arg-Met-Tyr; Tyr-Ala-Ala-Leu-Asp -Leu-Asn-Ala-Val-Ala-Asn-Lys-Ile -Ala-Asp-Phe-Glu-Leu; Tyr-Arg-Ala-Leu-Val-Asp -Thr-Leu-Lys-Phe-Val-Thr-Glu -Gln-Ala-Lys-Gly-Ala; and Tyr-Arg-Ala-Leu -Val-Asp-Thr-Glu-Phe-Lys-Val-Lys-Gln -Glu-Ala-Gly-Ala-Lys

The peptides may comprise an amphiphillic domain of apolipoprotein A-I and have a net charge of -2 or greater; they are soluble in water and plasma. Also claimed are peptides (again with a net charge of at least -2), which are derived from a vascular-associated protein such as elastin. The peptide may also contain a radioactive label which can be <sup>131</sup>I, <sup>125</sup>I, <sup>111</sup>In, <sup>99m</sup>Tc, <sup>203</sup>Pb, <sup>198</sup>Hg, <sup>97</sup>Ru or <sup>201</sup>Tc. Alternatively the label is a paramagnetic contrast agent.

USE/ADVANTAGE - (I) have an affinity for and a tendency to accumulate at a site of vascular injury. They can be used to diagnose vascular injury or disease or to inhibit the binding of LDL to vascular walls in the treatment of atherosclerosis. Administration may be oral or by arterial or venous injection. For diagnostic purposes, dosage is 0.5-1 mg/i.v. or 5-100 mg orally. For treatment of vascular disease, dosage is 5-100 mg i.v. or i.m.

Dwg.0/8

=> file home

FILE 'HOME' ENTERED AT 15:58:38 ON 15 MAR 2004

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using frame\_plus\_p2n model

March 12, 2004, 19:55:37 ; Search time 8134.53 Seconds  
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US-09-976-740-43

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

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Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: em\_hcc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_hcc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

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16: em\_estom.\*

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27: em\_gss\_vrl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have  
score greater than or equal to the score of the result being  
and is derived by analysis of the total score distribution.

# SUMMARIES

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6	1217	42.7	707	10	BE748961	BE748961
7	1211	42.5	743	10	BF058118	BF058118
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9	1189	41.7	683	10	BE857956	BE857956
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11	1166	40.9	774	10	BE891267	BE891267
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33	891	31.3	512	10	AW515766	AW515766
34	888	31.2	509	9	AI632586	AI632586
35	869	30.5	495	9	AI199022	AI199022
36	868	30.5	572	12	BM697252	BM697252
37	866	30.4	487	9	AI186705	AI186705
38	862	30.2	501	9	AI796089	AI796089
39	858	30.1	531	13	BX527955	BX527955
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ACCESSION BUI74966  
VERSION BUI74966.1 GI:22688950  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom  
REFERENCE 1 (bases 1 to 996)

http://mgs.nci.nih.gov/  
al Institutes of Health, Mammalian Gene Collection (MGC)  
ished (1999)  
t: Robert Strausberg, Ph.D.  
cgabbs-remail.nih.gov  
Procurement: ATCC  
Library Preparation: Rubin Laboratory  
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
Sequencing by: Agencourt Bioscience Corporation  
Distribution: MGC clone distribution information can be  
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Site\_2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed  
by Ling Hong in the laboratory of Gerald M. Rubin  
(University of California, Berkeley) using ZAP-CDNA  
synthesis kit (Stratagene) and Superscript II RT (Life  
Technologies). Note: this is a NIH\_MGC Library."

4.55e-29 Length: 996  
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city: 95.47% Mismatches: 6  
45.93% Indels: 3  
13 Gaps: 1

(1-538) x BU174966 (1-996)

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QY 434 GGLYsProAlaLeuProGlyAlaAspGlyThrProPheGlyCysProProGlyA

Db 475 GGCAACACGAGCCCTACCTGGGCGCCGACGGGACCCCTTTGGCTGTCTCCCGGGC

QY 454 GGLYsProSerAspProValGluTrpThrValMetAspValValGluTrpPheT

Db 535 GAGAGCCATCTGATCCGTCGAGTGGACCGTGATGATGTCGTCCTCAATATTTA

QY 474 AlaGlyPheProGluGlnAlaThrAlaPheGlnGluGlnGluAlaAspGlyLysS

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QY 533 aAspGlyPheLeu 537

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RESULT 2

LOCUS B0671165

DEFINITION BQ671165 921 bp mRNA linear EST 1

ACCESSION AGENCOURT\_8032664 NIH\_MGC\_102 Homo sapiens cDNA clone IMA

VERSION BQ671165.1 GI:21781999

KEYWORDS 5', mRNA sequence.

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 921)

AUTHORS NIH-MGC http://mgs.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information c  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM2379 row: 0 column: 17  
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Site\_2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using  
following 5' adaptor: GGCACGAG(G). Library cons  
by Ling Hong in the laboratory of Gerald M. Rubi  
(University of California, Berkeley) using ZAP-  
synthesis kit (Stratagene) and Superscript II RT  
Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:

5.59e-28	Length:	921
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ty: 93.98%	Conservative:	3
arity: 92.86%	Mismatches:	12
Indels: 44.56%	Indels:	4
13	Gaps:	1

(1-538) x BQ671165 (1-921)

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aLeuAlaLeuProArgGlyAspArgProGlyArgAlaProProAlaAlaSerAlaArg 313  
:::GCTTGGCTGCCCCGGGGACAGGCCCGAGCGGGCGCCGCCCGCCAGCGCCCGC 120  
oSerArgSerLyArgGlyGlyGluGluArgValLeuGluLyLeuGluGluGluAsp 333  
GTCTCGCAGCAAGAGAGTGTGGAGAGAGCGAGTACTTGAGAAAGAGAGAGAGAGAT 180  
pAspGluAspGluAspGluGluAspValSerGluGlySerGluValProGluSer 353  
T-----GATGAAGATGAAGAAGATGATGTGTGAGAGGGCTCTGAAGTGCCGAGAGT 234  
pArgProAlaGlyAlaGlnHisGlnLeuAsnGlyGluArgGlyProGlnSerAla 373  
CGGTCTGTCAGGTGCCAGCACCAACAGCTTACCGCGAGCGGGAGCCTCAGAGTGCC 294  
sGluArgValLyLeuGluTrpThrProCysGlyProHisGlnGlyAlaAspGluGlyArg 393  
GGAGAGGGTCAAGGAGTGGACCCCTCGCGACCGCACAGGGCCAGGATGAAGGGCGG 354  
yProAlaProGlySerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLySglu 413  
GCCAGCCCCGGGCGAGCGGCGCACCCGCCAGGTGTTCTCCATGGCAGCCATGAACAAGAA 414  
yGlyThrAlaSerValAlaThrGlyProAspSerProSerProValProLeuProPro 433  
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yLyProAlaLeuProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLyS 453  
CAAAACAGGCCTTACTTGGGCGCAGCGGACCCCTTTGGTGTCTCTCCGGGCGCAAA 534  
uLySProSerAspProValGluTrpThrValMetAspValValGluTyPheThrGlu 473  
GAGACCATCTGATCCCGTCAAGTGGACCGGTGATGGATGTCGTGCAATATTTTACTGAG 594  
aGlyPheProGluGlnAlaThrAlaPheGlnGluGlnGluIleAspGlyLySserLeu 493  
TGGATTCCCGGAGCGGCGACAGCTTTCACAGAGCAGGAAATTTGATGGCAAACTTTTG 654  
uLeuMetGlnArgThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeu 513  
GCTCATGCAGCGCGGATGTGCTTCCGGGGCTGTTTCATCGCCCTCGGGGCAACCCCTG 714  
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:::ATTCTACGATCACAGATCAAGGGCTTTTCGACAGGGCCCCCTTTGAGGGGTGATGACC 774  
AspGlyPheLeu 537  
:::GAGGGCTTCTTA 788

4500 828 bp linear EST 20-SEP-2000  
90248F1 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:3944674 5',  
sequence.  
4500  
4500.1 GI:10215698

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute- Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom- 1 (bases 1 to 828)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collector
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a> Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">image.llnl.gov</a> Plate: LLCW801 row: 0 column: 11 High quality sequence stop: 729.

FEATURES source

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Location/Qualifiers
1. 828
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3944674"
/issue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI
ECORI; cDNA made by oligo-dT priming. Directly
cloned into ECORI/XhoI sites using the following
adaptor: GGCACGAG(G). Size-selected 5500bp for
insert size 1.9kb. Library constructed by Ling
at the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis
(Stratagene) and Superscript II RT (Life Technol

```

## ORIGIN

Alignment Scores:			
Pred. No.:	3.36e-27	Length:	828
Score:	1241.50	Matches:	251
Percent Similarity:	95.49%	Conservative:	3
Best Local Similarity:	94.36%	Mismatches:	9
Query Match:	43.56%	Indels:	2
DB:	10	Gaps:	2
US-09-976-740-43 (1-538) x BE794500 (1-828)			
Qy	261	SerGlyGlyAlaGlyArgLeuThrArgGlyArgValGlnGlyLeuGlnGly	
Db	3	AGCGCGCGCGCGCGGTGCGCTTAACGCGCGCGGTGCA---GGGTGCTGGAC	
Qy	281	AlaAlaAArgGlyArgLeuGluArgThrArgLeuGlyAlaLeuAlaLeuPrc	
Db	60	CGCGCGGCTCGAGCCGCTCTGAGCGCACCGGTCTCGAGCGCTTGGCGTGGCC	
Qy	301	AspArgProGlyArgAlaProProAlaLaSerAlaArgProSerArgSerIys	
Db	120	GACAGCGCGAGCGGCGCGCGCGCGCGCGCGCGCGCGCTCTCGCAGCAAC	
Qy	321	GlyGluGluArgValLeuGlnLysGluGluGluGluAspAspAspGlnAspGlt	
Db	180	CGAAGAAGCGAGTACTTCAGAAAGAAAGAGGAGAGATGATGATCAAGATGAA	
Qy	341	GluAspAspValSerGluGlySerGluValProGluSerAspArgProAlaGly	
Db	240	GAAGATGATGTGTCAGAGGCTCTGAAGTGCCCGAGAGTGACCGTCTCGAGGT	
Qy	361	HisHisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLys	
Db	300	CACCACAGCTTAAACGGCGAGCGGGAGCTCAGAGTGCACAGAGAGGGGTCAAG	
Qy	381	ThrProCysGlyProHisGlnGlnAspGluGlyArgGlyArgProAlaArgProGly	

|||||  
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 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGly 440  
 GGGCCAGACTCCCGCTCCCGTCTTTCGCCCCAGCAACAGCCCTACCTGGG 539  
 AspGlyThrProPheGlyCyProProGlyArgLysGluLysProSerAspProVal 460  
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 sValLeuGlnGln 525  
 GGTGCTTCAGCAG 789

805 1109 bp mRNA linear EST 13-JUL-2000  
 3804F1 NIH\_MGC\_8 Homo sapiens cDNA clone IMAGE:2966449 5',  
 sequence.

805  
 805.1 GI:9144449

sapiens (human)

yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ases 1 to 1109)

MC http://mhc.nci.nih.gov/.

nal Institutes of Health, Mammalian Gene Collection (MGC)

lished (1999)

ct: Robert Strausberg, Ph.D.

: CGAPs-remail.nih.gov

ie procurement: Louis M. Staudt, M.D., Ph.D.

Library Preparation: Ling Hong/Rubin Laboratory

Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing by: Incyte Genomics, Inc.

ie distribution: MGC clone distribution information can be

i through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

: LNC69 row: h column: 02

quality sequence stop: 749.

Location/Qualifiers

1. .1109

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2966449"

/tissue\_type="Burkitt lymphoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 8"

/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technol

ORIGIN  
 Alignment Scores: 9.81e-27 Length: 1109  
 Pred. No.: 1229.00 Matches: 229  
 Score: 1229.00 Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 43.12% Gaps: 0  
 DB: 10

US-09-976-740-43 (1-538) x BE270805 (1-1109)

QY 310 AlaSerAlaArgProSerArgSerLysArgGlyGlyGluGluArgValLeuGlu  
 Db 3 GCCAGCGCCCGCCCTCTCCAGCAGAGAGAGTGGAGAGCGGAGTACTTGAG  
 QY 330 GluGluGluAspAspGluAspGluAspGluGluAspValSerGluGly  
 Db 63 GAGGAGAGAGATGATGATGAAGATGAAGATGAGAGAGATGATGTTCAGAGGCT  
 QY 350 ValProGluSerAspArgProAlaGlyAlaGlnHisGlnLeuAsnGlyGlu  
 Db 123 GTCCCCGAGAGTCACTCTGAGGTGCCAGCACCAGCTTAACGGCGAG  
 QY 370 ProGlnSerAlaLysGluArgValLysGluTyrThrProCysGlyProHisGln  
 Db 183 CCTCAGAGTCCCAAGAGAGAGGTCAAGAGTGGACCCCTCGGACCGCACCAG  
 QY 390 AspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValPheSerMet  
 Db 243 GATGAAGGGCGGGCGCCAGCCCGGGCAGCGGCGCAGCCCGCAGGTGTTCCTCATC  
 QY 410 MetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSerProSer  
 Db 303 ATGAACAAGGAAGGGGAAACAGCTTCTGTGGCCACCGGGCCAGACTCCCGTCTC  
 QY 430 ProLeuProGlyLysProAlaLeuProGlyAlaAspGlyThrProPheGly  
 Db 363 CCTTTGCCCGCGGCAACCCAGCCCTTACTGGGGCGGCGGACCCCTTTGGC  
 QY 450 ProGlyArgLysGluLysProSerAspProValGluThrValMetAspVal  
 Db 423 CCGGGCGCAAGAGAGAGCCATCTGATCCCGTCGAGTGGACCCGCTGATGGATGTC  
 QY 470 TyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGluGln  
 Db 483 TATTTTACTGAGGCTGGATTCCCGGAGCAGCGGACAGCTTTCGAAGAGCAGGAA  
 QY 490 GlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSerIle  
 Db 543 GGCAAACTTTGCTGCTCATGCAGCGCACAGATGTGCTCACCGGCTGTCTCATC  
 QY 510 GlyProAlaLeuLysIleTyrGluHisIleLysValLeuGlnGlnGlyHis  
 Db 603 GGGCCAGCCCTGAAATCTACGAGCACCACATCAAGGTGTTCAGCAAGGCCAC  
 QY 530 AspAspAspProAspGlyPheLeuGly 538  
 Db 663 GATGATACCCCGATGGCTTCTTAGGC 689

RESULT 5

BF058975

LOCUS

DEFINITION

BF058975

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute

BF058975 704 bp mRNA linear EST

7k36f08.x1 NCI CGAP Ov18 Homo sapiens cDNA clone IMAGE:3;

similar to FR:076866 076866 EG:100G10.6 PROTEIN. [1]; con

element MER22 repetitive element ; mRNA sequence.

BF058975

BF058975.1 GI:10812871

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute

alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 bases 1 to 704)  
 CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 onal Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 r Gene Index  
 blished (1997)  
 act: Robert Strausberg, Ph.D.  
 l: cgapbs-r@mail.nih.gov  
 ue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 mmet-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento  
 es, Ph.D. cDNA Library Arrayed by: Christa Prange, The  
 A.G.E. Consortium DNA Sequencing by: Washington University  
 me Sequencing Center  
 ne distribution: NCI-CGAP clone distribution information can be  
 d through the I.M.A.G.E. Consortium/LLNL, send email to:  
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 primer: -40UP from Gibco  
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 /lab\_host="DH10B (phage-resistant)"  
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 TGTTACCAATCTGAGTGGAGCGCGCGGCACATTTTTTTTTTTTTT 3'];  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not  
 I and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

Length: 704  
 Matches: 231  
 Conservativity: 1  
 Mismatches: 2  
 Indels: 0  
 Gaps: 0

(1-538) x BF058975 (1-704)

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 rAlaArgProSerArgSerLysArgGlyGlyGluGluArgValLeuGluLysGluGlu 330  
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Db 363 GAAGGGCGGGGGCGAGCCCGGGCAGCGGCACCGCGAGGTCTTCTCATGGC  
 QY 411 ASnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSerProSerPn  
 Db 423 AACAGGAGGGGGAACAGCTTCTGTTCACCGGGCCAGACTCCCGTCCCC  
 QY 431 LeuProGlyLysProAlaLeuProGlyAlaAspGlyThrProPheGlyCY  
 Db 483 TTGCACCCAGGCAACACAGCCCTACCTGGGGCCGAGCGGACCCCTNTGGCTG  
 QY 451 GlyArgLysGluLysProSerAspProValGluTrpThrValMetAspValva  
 Db 543 GGCGCAAGAGAGAGCATCTGATCCCGTCGAGTGGACCGTGGATGTCGT  
 QY 471 PheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGluGlnLui  
 Db 603 TWTACTGATGCTGGATTCCCGGAGCAGCGAGCTTCTTCCAGAGCAGGAAT  
 QY 491 LysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGly 504  
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## RESULT 6

BE746961

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. 707

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3929733"

/tissue\_type="adenocarcinoma cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 9"

/notes="Organ: ovary; Vector: pOTB7; Site 1: Xho"

EcoRI, cDNA made by oligo-dT priming. Directly

cloned into EcoRI/XhoI sites using the following

adaptor: GGCACGAG(G). Size-selected &gt;500bp fo

insert size 1.8kb. Library constructed by Ling

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis

(Stratagene) and Superscript II RT (Life techn

## ORIGIN

Alignment Scores:

Pred. No.: 1,48e-26 Length: 707

Score: 1217.00 Matches: 229

Percent Similarity: 99.14% Conservativity: 2

Best Local Similarity: 98.28% Mismatches: 2





**us-09-976-740-43.rst**

[illegible]

COMMENT: Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information (c)  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 plate: LLCM1866 row: h column: 15  
 High quality sequence stop: 785.

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 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NLTH MGC 8"  
 /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; EcoRI; cDNA made by oligo-dT priming. Direction: cloned into EcoRI/XhoI sites using the following adaptor: GCACGAG(G). Size-selected >500bp for insert size 1.8kb. Library constructed by Ling at the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis (Stratagene) and Superscript II RT (Life Technol.

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 Percent Similarity: 98.73% Conservative: 0  
 Best Local Similarity: 98.73% Mismatches: 3  
 Query Match: 41.44% Indels: 3  
 DB: 12 Gaps: 0

US-09-976-740-43 (1-538) x BI226646 (1-785)

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424 4543F1 NIH\_MGC\_8 Homo sapiens linear EST 15-AUG-2000  
 sequence. IMAGE:3677194 5',  
 424

424.1 GI:9805144

sapiens (human)

sapiens

yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ases 1 to 858)

GC http://mgc.nci.nih.gov/.

nal Institutes of Health, Mammalian Gene Collection (MGC)

lished (1999)

ct: Robert Strausberg, Ph.D.

: cgsaps-r@mail.nih.gov

e Procurement: Louis M. Staudt, M.D., Ph.D.

Library Preparation: Ling Hong/Rubin Laboratory

Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing by: Incyte Genomics, Inc.

e distribution: MGC clone distribution information can be

through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

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quality sequence stop: 709.

Location/Qualifiers

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3677194"

/tissue\_type="Burkitt lymphoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_8"

/note="Organ: lymph; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCAGGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

1.08e-24 Length: 858  
 1154.50 Matches: 223  
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 98.67% Mismatches: 3  
 40.51% Indels: 2  
 10 Gaps: 0

(1-538) x BE561424 (1-858)

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AGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 121

iProGluSerAspArgProAlaGlyAlaGlnHisHisGlnLeuAsnGlyGluArgGly 369

3CCGAGAGTGACCGTCTCGAGTCCCGACGACCCACAGCTTAACGGCGAGCGGGA 181

xGlnSerAlaLysGluArgValLysGluTrpThrProCysGlyProHisGlnGln 389

Db 182 CCTCAGAGTCCAGGAGAGGGTCAAGAGTGGACCCCTCGGACCGCACCA-  
 Qy 390 AspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValPheSerMetP  
 Db 241 GATGAAGGGGGGGGGCCAGCCCGGGGCGAGCGGACCCGCGAGGTGTCTCATGC  
 Qy 410 MetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSerProSerf  
 Db 301 ATGAACAGAGAGGGGAGACAGCTTCTGTGGCCACCGGGGCGAGCTCCCGTCC  
 Qy 430 ProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrProPheGlyC  
 Db 361 CCTTTGCCCCAGGCAAAACAGCCCTACCTGGGGCGAGCGGACCCCTTTGGCT  
 Qy 450 ProGlyArgLysGluLysProSerAspProValGluTrpThrValMetAspVal  
 Db 421 CCCGGGCGCAAGAGAGCCATCTGATCCCGTCCAGTGGAGCCCGTATGGATGCC  
 Qy 470 TysPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGluGlnGlu  
 Db 481 TATTTTACTGAGGCTGGATTCCCGGAGCAGCGGACAGCTTTCCAGAGCAGGAA  
 Qy 490 GlyLysSerLeuLeuMetGlnArgThrAspValValLeuThrGlyLeuSerIle/  
 Db 541 GGCAAAATCTTTGCTGCTCATGCGAGCGCACAGATGTGCTCACCGGCTGTC--ATC  
 Qy 510 GlyProAlaLeuLysIleTyGluHisHisIleLysValLeuGlnGlnGlyHis  
 Db 599 GGGCCAGCCCTGAAAATCTACGAGCACCACATCAAGGTGCTTTCAGCAGGCCAC  
 Qy 530 AspAspAspProAspGly 535  
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RESULT 13

BM554748

LOCUS

DEFINITION

BM554748 1057 bp mRNA linear EST ;

AGENCOURT 6545443 NIH\_MGC\_88 Homo sapiens

5', mRNA sequence.

BM554748 1 GI:18794615

VERSION

BM554748.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom

1 (bases 1 to 1057)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgsaps-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LHAM12746 row: f column: 07

High quality sequence stop: 557.

Location/Qualifiers

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5736966"

/tissue\_type="duodenal adenocarcinoma, cell line

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_88"

/note="Organ: small intestine; Vector: pCMV-SPO1

Site\_1: NotI; Site\_2: SalI; Cloned unidirection.

TTGAAGGATGATGACCCC 800

[illegible]

QY  
363 UGGLYGRUATL3011



GenCore version 5.1.6  
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leic search, using frame\_plus\_p2n model

March 12, 2004, 19:49:56 ; Search time 8171.41 Seconds

(without alignments)  
2853.675 Million cell updates/sec

US-09-976-740-43

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Ygapop 10.0 , Ygapext 0.5  
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Delop 6.0 , Delext 7.0

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hits satisfying chosen parameters: 6940544

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Minimum Match 0%  
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Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have  
score greater than or equal to the score of the result being  
and is derived by analysis of the total score distribution.

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5	2616.5	91.8	12425	6	AX239607	AX239607
6	2594	91.0	2560	4	AY453841	AY453841
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10	1560	54.7	1470	9	BC030129	BC030129
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12	1455.5	51.1	1617	6	AR374682	AR374682
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ALIGNMENTS



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A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
density lipoprotein binding proteins and their use in diagnosing  
treating atherosclerosis  
nt: WO 0164874-A 45 07-SEP-2001;  
on Heart Foundation, Inc. (US)

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3.26e-44 Length: 1614  
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 A.M., Deconinck, A.E., Campbell, B.D. and Lees, R.S.  
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 t Submission  
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 9 Gaps: 0

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 A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1
2 Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.
3 Low density lipoprotein binding proteins and their use in d
4 and treating atherosclerosis
5 Patent: WO 0164874-A 50 07-SEP-2001;
6 Boston Heart Foundation, Inc. (US)
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Joint Genome Institute and Stanford Human Genome Center.  
ct Submission  
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bases 1 to 237931  
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ct Submission  
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# KEYWORDS

## SOURCE

### ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo

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Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Sci  
Altschul,S.F., Zerborg,B., Buetow,K.H., Schaefer,C.F., Bi  
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsi  
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong  
Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,  
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,  
Carninci,P., Prange,C., Raja,S.S., Loquellano,N.A., Peter  
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,  
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,  
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,  
Villalob,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,F  
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Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,  
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Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., My  
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalilus,D.  
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A. full-  
generation and initial analysis of more than 15,000 full-  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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2 (bases 1 to 1470)

Strausberg,R.

Direct Submission

Submitted (07-MAY-2002) National Institutes of Health, M  
Gene Collection (MGC), Cancer Genomics Office, National C  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 2085  
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

On Aug 19, 2003 this sequence version replaced gi:2253961  
Contact: MGC help desk

Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramu  
Sequencing Center (NISC),  
Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>Contact: [nisc.mgc@nih.gov](mailto:nisc.mgc@nih.gov)

Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,F  
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brc  
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.  
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Lega  
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCLC  
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touc  
Youngson,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggi  
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information ca  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.1>  
Series: IRAL Plate: 15 Row: m Column: 17  
This clone was selected for full length sequencing becaus  
passed the following selection criteria: Hexamer frequenc  
analysis, Genomescan gene prediction.

Location/Qualifiers

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/clone="IMAGE:3943601"

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# FEATURES

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In many cases mediates homodimerisation"
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DEFINITION Sequence 11 from patent US 6355451.
ACCESSION AR199530
VERSION AR199530.1 GI:20249604
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1617)
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.
TITLE Low density lipoprotein binding proteins and their use i
JOURNAL Patent: US 6355451-A 11 12-MAR-2002;
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Alignment Scores:
Pred. No.: 3,47e-19 Length: 1617
Score: 1455.50 Matches: 281
Percent Similarity: 92.86% Conservative: 18
Best Local Similarity: 87.27% Mismatches: 13
Query Match: 51.07% Indels: 10
DB: 6 Gaps: 3

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ORGANISM		Oryctolagus cuniculus		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute		
AUTHORS		Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
TITLE		1		
JOURNAL		Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.		
FEATURES		Low density liprotein binding proteins and their use in		
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		Patent: WO 0164874-A 11 07-SEP-2001;		
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Best Local Similarity:		87.27%	Mismatches:	13
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444 1617 bp DNA linear PAT 27-AUG-2002  
 low density lipoprotein binding proteins and their use in  
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 low density lipoprotein binding proteins and their use in

diagnosing and treating atherosclerosis  
 Patent: JP 2001506983-A 2 29-MAY-2001;  
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 PN JP 2001506983-A/2  
 PD 29-MAY-2001  
 PF 26-NOV-1997 JP 1998524870  
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 Best Local Similarity: 87.27% Mismatches: 13  
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09:28:15 2004

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41 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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March 12, 2004, 19:48:14 ; Search time 852.766 Seconds  
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US-09-976-740-43

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Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: Geneseq2002s:\*

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9: Geneseq2003cs:\*

10: Geneseq2004s:\*

is the number of results predicted by chance to have a  
per than or equal to the score of the result being printed,  
lived by analysis of the total score distribution.

# SUMMARIES

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AC AAH26499;

XX

DT 12-NOV-2001 (first entry)

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DE Human low density lipoprotein binding protein 2 (LBP-2) DNA.

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KW Low density lipoprotein binding protein 2; LBP-2; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; ds.

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OS Homo sapiens.

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PN WO200164874-A2.

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PD 07-SEP-2001.

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PF 28-FEB-2001; 2001WO-US006356.

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PR 02-MAR-2000; 2000US-00517849.

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PR 14-JUL-2000; 2000US-00616289.

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(BOST-) BOSTON HEART FOUND INC.

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PI Lees AM, Lees RS, Law SW, Arjona AA;

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DR WPI; 2001-565505/63.

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P-ESDB; AAB82806.

low density lipoprotein binding polypeptide for treating, d/or identifying therapeutic agents for atherosclerosis.

7A; 143pp; English.

sequence is that of the coding region of the human gene (see p-2, see AAB82806). The gene was isolated from a genomic DNA LBP-2 cDNA as probe. The LBP-2 protein predicted from the sequence differs from that predicted from a cDNA clone (see that it contains an additional 321 amino acids at its N-terminus). LBP-2 nucleic acids are among the nucleotides of the invention that encode novel polypeptides corresponding to native and methylated LDL. Also claimed are polypeptides, and biologically active fragments and derivatives thereof, as well as expression vectors, cells and methods of using them. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in treating atherosclerosis, and methods for treating a cell having an abnormality in the metabolism of LBP are claimed. Pharmaceutical compositions containing LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed.

BP; 243 A; 638 C; 564 G; 169 T; 0 U; 0 Other;

```

2.04e-69      1614
2850.00%     538
100.00%
ity: 100.00%
100.00%
5
Length:
Matches:
Conservative:
Mismatch:
Indels:
Gaps:

```

1-538) x AAH26499 (1-1614)

laGlyProProAlaLeuProProGluThrAlaalaalathrThrAlaAla 20  
CGGGGCCCCGGGCCCTACCCCGCGAGACGGCGCGCGCCACCAACGGCGCG 60  
laSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuaspThrIleAsp 40  
CCTGTCGTCGCGCGCTTCCCGGCATCTACAGAGTGGATCTGGACACCATCGAC 120  
euArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetValArgArg 60  
TGCCTCGGCCAAGCGCGCGCGACCTCGAGCGCATCTGCCGATGGTGGCGCG 180  
isGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGlnArg 80  
ACGGCCGGAGCCGAGCGCACGGCGCGAGCTCGAGAACTGATCCAGACGCGC 240  
alIeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgValGln 100  
TGCTCCGGGTCACTACAAGGGAGCATCTCGTACCGCAACGCGCGCGCGTCCAG 300  
roArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyAlaProAla 120  
CCGGCGCGGAGCACCCCGCGGCCCGCGCGCGCCCGCGCGCGCGCGCCCGCG 360  
laAlaAlaAlaProProThrProAlaProProProProAlaProVal 140  
CCGCGCGCGCGCGCGCGCCACGCGCGCCCGCGCGCACGCGCCGCGCGCCGTC 420  
laAlaAlaProAlaArgAlaProArgAlaAlaAlaAlaAlaThrAlaProPro 160  
CCGGCGCGCCCG 480  
roGlyProAlaGlnProGlyProArgAlaGlnArgAlaAlaProLeuAlaPro 180  
CTGGCCCCGGCAGCGGGCCCCCGCGCGAGCGGGCCCGGCCCTTGGCGCGCGCG 540  
roAlaProAlaAlaProProAlaValAlaProProAlaGlyProArgArgAlaPro 200

## RESULT 2

RESUL 2  
AAH26495

AAH20493  
ID AAH26495 standard: DNA: 12425 BP.[illegible]

## RESULT 2

RESUL 2  
AAH26495

AAH20493  
ID AAH26495 standard: DNA: 12425 BP.

(first entry)

density lipoprotein binding protein 2 (LBP-2) gene.

lipoprotein binding protein 2; LBP-2; LDL; human;  
osis; arteriosclerotic; gene therapy; diagnosis; vaccine;

is.

Location/Qualifiers

2832..5153

/tag= a

/note= "includes introns"

2832..3785

/tag= b

3786..4207

/tag= c

4208..4502

/tag= d

4503..4593

/tag= e

4594..4694

/tag= f

4695..4787

/tag= g

4788..4899

/tag= h

4900..4994

/tag= i

4995..5153

/tag= j

-A2.

; 2001WO-US006356.

; 2000US-00517849.

; 2000US-00616289.

TON HEART FOUND INC.

ees RS, Law SW, Arjona AA;

55505/63.

82806.

low density lipoprotein binding polypeptide for treating,  
and/or identifying therapeutic agents for atherosclerosis.

Fig 23; 143pp; English.

Sequence is that of genomic DNA encoding novel human low  
protein binding protein 2 (LBP-2, see AAB82806). The DNA was  
from a human genomic library by screening with LBP-2 cDNA (see  
The open reading frame spans 5 exons. Human LBP-2 nucleic  
non claimed polynucleotides of the invention that encode  
epitopes, termed LBPs, capable of binding to native and  
LDL. Also claimed are isolated LBP polypeptides, and  
y active fragments and analogues of them, as well as  
vectors, cells and methods of producing the LBPs. Methods of  
if an animal is at risk for atherosclerosis, and methods for  
an agent for use in treating atherosclerosis, and methods for  
cell having an abnormality in structure or metabolism of LBP  
. Pharmaceutical compositions comprising an LBP polypeptide or  
d, and vaccine compositions, are also claimed

425 BP; 2563 A; 3702 C; 3566 G; 2594 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 1.35e-62 Length: 12425  
Score: 2616.50 Matches: 536  
Percent Similarity: 69.16% Conservative: 0  
Best Local Similarity: 69.16% Mismatches: 2  
Query Match: 91.81% Indels: 239  
DB: 5 Gaps: 4

US-09-976-740-43 (1-538) x AAB26495 (1-12425)

QY	1	MetAlaGlyProProAlaLeuProProGluThrAlaAlaAlaAlaThrTh:
Db	2832	ATGGCGGGGCGCGCGCGCTACCGCGCGGAGCGCGCGCGCGCGCGCAC
QY	21	AlaAlaSerSerSerAlaAlaSerProHisTyrGlnGluTyrIleLeuAspTh:
Db	2892	GCGCGCTCGTCTCGCGCGCGCTTCCCGCGCACTACCAAGAGTGGATCTTGGACAC
QY	41	SerLeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetVa:
Db	2952	TGGCTGGCTCGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY	61	ArgHisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGlr
Db	3012	CGGCG
QY	81	AlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaAr:
Db	3072	GCGGTGCTCGCGGTGAGCTACAGGGAGCGCTCTCGTACCGCAACCGCGCG
QY	101	ProProArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyAl:
Db	3132	CG
QY	121	AlaAlaAlaAlaAlaProProProThrProAlaProProProProProAla:
Db	3192	GCG
QY	141	AlaAlaAlaAlaProAlaArgAlaProArgAlaAlaAlaAlaAlaThrAl:
Db	3252	GCG
QY	161	SerProGlyProAlaGlnProGlyProArgAlaGlnArgAlaAlaProLeuAl:
Db	3312	TGGCTGGCG
QY	181	ProProAlaProAlaAlaProProAlaValAlaProProAlaGlyProArgAr:
Db	3372	CGCGCGCGCGCGCGCGCTCCCGCGCGTGGCGCGCGCGCGCGCGCGCG
QY	201	ProProAlaValAlaAlaArgGluProProLeuProProProProGlnProPr:
Db	3432	CGCGCGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY	221	ProGlnGlnGlnProProProProGlnProGlnProProProGlnGlyGly
Db	3492	CCACAGCAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY	241	ArgAlaGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrLeu
Db	3552	CG
QY	261	SerGlyGlyAlaGlyGlyArgLeuThrArgGlyArgValGlnGlyLeuLeuGlu
Db	3612	AGCGCGCGCGCGCGCGTGGCTAACCGCGCGCGCGCGCGCGCGCGCG
QY	281	AlaAlaAlaArgGlyArgLeuGluArgThrArgLeuGlyAlaLeuAlaLeuPro
Db	3672	GCGCGCGTGGCGCGCGTGGAGCGCACCGCTCTCGGAGCGCGTGGCGTGC
QY	301	AspArgProGlyArgAlaProProAlaAlaSerAlaAlaArgProSerArg----



normality in structure or metabolism of LBP. Pharmaceutical  
s comprising an LBP polypeptide or nucleic acid, and vaccine  
s, are also claimed

61 BP; 372 A; 937 C; 879 G; 373 T; 0 U; 0 Other;

2.13e-62 Length: 2561  
2594.00 Matches: 503  
Conservative: 17  
arity: 91.12% Mismatches: 16  
Indels: 16  
Gaps: 5

(1-538) x AAH26500 (1-2561)

taLaGlyProProAlaLeuProProGluThrAlaAlaAlaThrThr---Ala 19  
GGGGGGCCCCCGCCCTACCCCGCGGAGACGGCGCGGCCGCCACCGCGCGCG 305  
aAlaSerSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIle 39  
CGCGCCCTCGTCTGCTCGCGCTTCCCGGCACTACCAAGAGTGGATTCTGGACACCATC 365  
oSerLeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetValArg 59  
CTGCTCGCTCGCGCAAGCGCGCGCGACCTGGAGCGCATCTCGCGGATGTGTGGG 425  
jArgHisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGlnGln 79  
CGGACCGCGCGGAGCGGAGCGGCGCGCGCGCGGAGTCTCGAGAACTGATTCAGCG 485  
jAlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgVal 99  
CGCGTGTCTCGGCTCAGCTACAGGAGGAGCATCTGTTACCGCAACGCGCGCGCTC 545  
iProProArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyAlaPro 119  
CGCGCGCGCGCGGAGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 605  
iAlaAlaAlaAlaAlaProProProThrProAlaProProProProProAlaPro 139  
-----GCCG 659  
[---AlaAlaAlaAlaProAlaAlaProArg-----AlaAlaAlaAlaAla 156  
XGCG 719  
AlaProProSerProGlyProAlaGlnProGlyProArgAlaGlnArgAlaAlaPro 176  
AGCG 779  
iAlaAlaProProAlaProAlaAlaProProAlaValAlaAlaProProAlaGlyPro 196  
XGCG 839  
jArgAlaProProPro-----AlaValAlaAlaArgGluProProProProPro 214  
XGCG 899  
XGlnProProAlaProGlnGlnGlnGln-----ProProProProPro 229  
XAGCG 959  
iProGlnProProProGluGlyAlaValArgAlaGlyGlyAlaAlaArgProVal 249  
XCACAGCG 1019  
LeuArgGluValValArgTyrLeuGlyGlySerGlyGlyAlaGlyGlyArgLeuThr 269  
XTCGCGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079  
jGlyArgValGlnGlyLeuLeuGluGluAlaAlaAlaArgGlyArgGlyLeuArg 289

1080 CGCGCGCGCGTGCAGGGTCTGCTGGAAGAGAGGCGCGCGCGCGCGCGCGCTK  
QY ThrArgLeuGlyAlaLeuAlaLeuProArgGlyAspArgProGlyArgAlaPro  
1140 ACCGCTCTCGAGGCGCTTGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG  
QY 310 AlaSerAlaArgProSerArgSerLysArgGlyGlyGluGluArgValLeuGlu  
1200 GCCAGCG  
DB 330 GluGluGluAspAspGluAspGluAspGluAspGluAspGluAspGluAsp  
QY 1260 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
DB 348 SerGluValProGluSerAspArgProAlaGlyAlaGlnHisGlnLeuSer  
1320 TCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
DB 367 GluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThrProCysGly  
QY 1380 GAGCG  
DB 387 GlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnVal  
QY 1440 CCTGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
DB 407 MetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProSer  
QY 1500 ATGCGCGCGCTTGGTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
DB 427 SerProValProLeuProGlyLysProAlaLeuProGlyValAlaAspGlyThr  
QY 1560 TCCCGCGTGCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTC  
DB 447 GlyCysProProGlyArgGlyGlyLysProSerAspProValGluTrpThrVal  
QY 1620 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
DB 467 ValValGluTrpPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGln  
DB 1680 GTCGTGGAGTACTTCCCGAGCGCGCTTCCCTGAGCAAGCCCGCGCTTTCAG  
QY 487 GluIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGly  
DB 1740 GAGATCGAGCGCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
QY 507 IleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGln  
DB 1800 ATCCGCTTGGCGCGCGCGTGGAAATCTATGAGCACCACATATCAGGTGCTG  
QY 527 HisPheGluAspAspProAspGlyPheLeuGly 538  
DB 1860 CACTTCAGGAGCAGTATGATCCCGAAGGCTTCTCTGGGA 1895

RESULT 4

AAH26488  
ID AAH26488 standard; cDNA; 1617 BP.  
XX AAH26488;  
AC AAH26488;  
DT 12-NOV-2001 (first entry)  
XX Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.  
DE Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;  
KW atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis;  
KW ss.  
XX Oryctolagus cuniculus.  
OS  
XX Key Location/Qualifiers  
FH 1.955  
FT CDS

```

/*tag= a
/partial
/Note= "includes in-frame stop codon at nucleotides
28..30"

12.

2001WO-US006356.
2000US-00517849.
2000US-00616289.
DN HEART FOUND INC.

as RS, Law SW, Arjona AA;
5505/63.
2798.

low density lipoprotein binding polypeptide for treating,
id/or identifying therapeutic agents for atherosclerosis.

ig 11; 143pp; English.

sequence is that of cDNA encoding a portion (see AAB82798) of
low density lipoprotein binding protein 2 (LBP-2). The cDNA
following screening of a rabbit cDNA library for clones
that bound to both native low density lipoprotein (LDL) and
a full-length sequence for LBP-2 is given in AAB26500. The
divides claimed polynucleotides encoding novel polypeptides
capable of binding to native and methylated LDL, the isolated
termed LBPs, and biologically active fragments and
them, as well as expression vectors, cells and methods of
LBPs. Also claimed are methods of determining if an animal
or atherosclerosis, methods for evaluating an agent for use
atherosclerosis, and methods for treating a cell having an
in structure or metabolism of LBP. Pharmaceutical
comprising an LBP polypeptide or nucleic acid, and vaccine
, are also claimed

7 BP; 289 A; 513 C; 530 G; 285 T; 0 U; 0 Other;

7-73e-32 Length: 1617
Matches: 281
Conservative: 18
Mismatch: 13
Indels: 10
Gaps: 3

(1-538) x AAB26488 (1-1617)

AlaGlnGlnProProProGlnProGlnProPro-GluGlyGlyAlaVa 240
AGCAGCAGCAA-----CAACCGCTAGCCGAGGAGGTGGCGCGC 47
AlaGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrLeuGlyG 260
AGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 107
GlyGlyAlaGlyGlyArgLeuThrArgGlyArgValGlnGlyLeuLeuGluGlu 280
CAGCGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 167
AlaAlaArgGlyArgLeuGluArgThrArgLeuGlyAlaAlaAlaLeuProArgG 300
AGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 227
ArgProGlyArgAlaProProAlaAlaSerAlaArgProSerArgSerArgG 320
AGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 287

```

```

QY 320 yGluGluArgValLeuGluGlyGluGluGluGluGluGluGluGluGluGlu
DB 288 TGGCGAGGAGCGAGTGTCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG
QY 340 uGluAspAsp-----ValSerGluGlySerGluValProGluSerAspArgPro
DB 348 CGACGACGACGACGTCGTGTCCGAGGGCTCGGAGGTGCCGAGAGCGATCGTCCC
QY 358 yAlaGlnHisHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaGlyGlu
DB 408 TGGCAGCATCACCACTGAATGGCGGCGAGCGCGCGCGCGCGCGCGCGCGAG
QY 377 llyGluTrpThrProCysGlyProHisGlnGlnAspGluGlyArgGlyPro
DB 468 CAAGGAGTGTCTGTGTGTGGCCCCCACCCTGCGCCAGGAGGAGGCGCGGGCGG
QY 397 oGlySerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGly
DB 528 GGGCAGTGGCACCCCGCCAGGTCTTCTCCATGGCGGCTTTGAGTAAGGAGGGGGA
QY 417 aSerValAlaThrGlyProAspSerProSerProValProLeuProProGlyLys
DB 588 CTTCTGACCAACCGGCGCTGACTCCCGTCCCGGTGCTGCTTGGCCCCCGGAG
QY 437 aLeuProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGluLys
DB 648 CCTCCAGGAGCGGATGGGACCCCTTTGGTGCCTCGCGCGCGCGCAAGAGAG
QY 457 rAspProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGly
DB 708 AGACCCCGTGGAGTGACAGTATCGAGCGTCTGTGAGTACTTTCACGAGCGCGG
QY 477 oGluGlnAlaThrAlaPheGlnGluGlnLeuLeuAspGlyLysSerLeuLeu
DB 768 TAGCAGCAGCAGCGCTTTCAGGAGCAGGAGATCGAGGCAAGTCTCTGCTGTC
QY 497 nArgThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIle
DB 828 GCGCACCGAGTGTCTCACCGGCTGTCCATCGCGCTGGGGCGGCGGTTGAAAAATC
QY 517 uHisIleIleValLeuGlnGlnGlyHisPheGluAspAspAspProAspGly
DB 888 GCACCATATCAAGGTGCTGCAGCGGTCACTTCGAGGACGATGACCCCGGAGGCG
QY 537 uGly 538
DB 948 GSGA 951

RESULT 5
AAV32835
ID AAV32835 standard; cDNA; 1617 BP.
XX AAV32835;
XX 09-NOV-1998 (first entry)
XX Rabbit low density lipoprotein binding protein LBP-2 cDNA.
XX Low density lipoprotein binding protein; LDL binding protein 2;
XX receptor; rabbit; atherosclerosis; diagnosis; therapy; vaccine;
XX Oryctolagus cuniculus.
XX Key Location/Qualifiers
XX CDS 1..954
XX /tag= a
XX misc_feature 156..1617
XX /tag= b
XX /note= "Claim 5"
XX misc_feature 156..954
XX /tag= d
XX /note= "Claim 6"
FT

```



121 GAAGATGAAGAAGATGATGTGCAGAGGCTCTGAAGTCCCGAGAGTGACCGTC  
358 GlyAlaGlnHisHisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluA  
181 GGTGCCCAACGACACACAGCTTAAACGCGAGCGGGACCTCAGAGTGTCCAAGAGA

241 AAAGGHG TGGAC CCCC TGGGAC CGCAC CAGGG CCHAGGA TGAHGG GCAGGG GC CAG

301 GGCAAGCGCACCGCCAGGCTGTTCTCTCAATGGCAGCCATGATCAATGGAATGGGGAA

[illegible]

TGCTTGGTCACCGAGATCCCGTCCCCGTGCCTTGCTCCTTGGCTTTGGCCCTCAAGGCCAATAC

438 DEUTIOGLYALASPGLYINTFIOFNEGUCYBFIOTIOGLYHIGLYSGIULYSF

421 CTAACCTGGGCTCAGACCGGACCCCTTGGCTGTCTCCCGGCGCAGAAAGAGAGG

458 AspProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyP

481 GATCCGTCGAGTGGACCGATGGATGCTGCGAATATTTACTGAGCGTGGAT  
478 GluGlnAlaThrAlaPheGlnGluGlnGluIleAspGlySerLeuLeuLeuM

**TITLE**

490 ALGGINADPVALDENHINOLYDEUQSEIRIKALYDEUSLYFIALADENMYSALIC  
601 CGCACAGATGTGCTCACGGGCGCTGTCCATCCGCGCTCGGGCCAGCCCTGAAAAATCT  
518 HIEHIEIIELYSEVALLIEUGLNGLNHISPhEGluAspAspProAspGlyP  
661 CACCACATCAAGGTGCTTCAGCAAGGCCACTTTGAGGATGATGACCCCGATGGCT  
538 Gly 538  
721 GGC 723  
490 standard; cDNA; 1422 BP.  
490;  
IV-2001 (first entry)

t low density lipoprotein binding protein 3 (LBP-3) cDNA.

Location/Qualifiers
1. 955

**\*tag= a**  
**/partial**

164874-A2.  
P-2001.

B-2001; 2001WO-US006356.  
R-2000: 2000US-00517849.

T-2000; 200005-0001020203;

ees RS, Law SW, Arjona AA;

82800.

Fig 13; 143pp; English.

22 BP; 265 A; 447 C; 442 G; 268 T; 0 U; 0 Other;

(1-538) x AAH26490 (1-1422)

rArgLeuGlyAlaLeuAlaLeuProArgGlyAspArgProGlyArgAlaProProAla 309  
CGCTCTCGAGAGCGCTTTCGCTGCTCCCGCGGGGACAGCGCCGGACCGGGCC 60  
aSerAlaArgProSerArgSerIysArgGlyGlyGluGluArgValLeuGluLysGlu 329  
TAGCGCCCGCGCGCGGACCAAGAGAGCTGCGAGGACGAGTCTTGAAGAAGGAG 120  
gGluGluAspAspAspGluAspGluAspGluGluAspAsp-----ValSerGluGly 347  
GAGAGGAGGAGGAGGAGGAGACACGACGAGGACGACGACGAGCTGTGTCGAGGGC 180  
rGluValProGluSerAspArgProAlaGlyAlaGlnHisGlnLeuAsn---Gly 366  
GAGAGTGCCCGAGAGCGATCTGTCGCGGGTGGCAGCATCACAGCTGAATGGCGGC 240  
rArgGlyProGlnSerAlaLysGluArgValLysGluTrpThrProCysGlyProHis 386  
GCGCGCGCCGCGACCGCCAAAGAGCGGGCCAGGAGTGTGCTGTGGCCCCCAC 300  
gGlyGlnAspGluGlyValArgGlyProAlaProGlySerGlyThrArgGlnValPheSer 406  
TGCCAGAGAGAGAGGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGAGGTGTCTCC 360  
rAlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSerPro 426  
GCGCGCTTGTAGTAAGGAGGGGGGATCAGCTCTTCGACCAACCGGGCGCTGACTCCCG 420  
rProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrProPhe 446  
CCGGTGGCTTTTGCCCCCGGGGAAGCAGCGCTCCCGAGGAGCGGATGGGACCCCTTT 480  
rCysProProGlyValGlyLysGluLysProSerAspProValGluTrpThrValMetAsp 466

Standard: cDNA: 1208 BP.

QY 342 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaG



ATCGAGCGCAAGTCCCTGCTGCTCATGACGCGACCGATGTCCTCACCAGCTGTGCC 600  
 ArgLeuGlyProAlaLeuLysIleTyrGluHisIleValLeuGlnGly 526  
 XGCTGGGCGCCAGTGGTGAATCTATGACCATATCAAGTGTCTGACAGGCT 660  
 PheGluAspAspAspProAspGlyPheLeuGly 538  
 TCGAGGACGATGACCGCGAAGGCTTCTCTGGGA 696

idard; cDNA; 1134 BP.

(first entry)

id protein gene 9 SEQ ID NO:19.

ed protein; diagnosis; neuroprotective; cytostatic;  
 al; immunomodulatory; muscular active general; vulnary;  
 inal; nephrotropic; antiinfective; gynaecological;  
 rial; gene therapy; detection; cancer; chromosome marker;  
 lentification; neural disorder; immune disorder;  
 order; reproductive disorder; gastrointestinal disorder;  
 order; cardiovascular disorder; renal disorder;  
 disorder; wound healing; infectious disease; preservative;  
 ; 88.

1.

2000WO-US0006822.

99US-0126054P.  
 99US-0169916P.

GENOME SCI INC.

iben SM, Komatsoulis G;  
 7666/55.  
 1307.

ed proteins and gene sequences encoding them, useful for  
 reventing, and treating disorders such as cancer,  
 disorders and immune system disorders.

344; 429pp; English.

sotide sequences given in AAC59566 to AAC59614 encode the  
 ed proteins given in AAB34299 to AAB34347. AAB34348 to  
 resent human secreted polypeptide sequences and proteins  
 them, which are given in the exemplification of the present  
 man secreted proteins have activities based on the tissues  
 genes are expressed in. Example of activities include:  
 ive; cytostatic; cardiactive; immunomodulatory; muscular;  
 al; vulnary; gastrointestinal; nephrotropic; antiinfective;  
 al; and antibacterial. The polynucleotides can be used for  
 n of various disorders such as cancer, chromosome  
 on, as chromosome markers, and for numerous other diagnostic  
 purposes. The secreted proteins can be used to treat  
 ch as neural, immune, muscular, reproductive,  
 inal, pulmonary, cardiovascular, renal, and proliferative  
 und healing, and infectious diseases. The proteins can also  
 food additive or preservative to increase or decrease  
 bilities. AAC59557 to AAC59565 and AAB34298 represent  
 ed in the exemplification of the present invention

SQ Sequence 1134 BP; 248 A; 294 C; 366 G; 225 T; 0 U; 1 Other;

Alignment Scores:  
 Pred. No.: 1,46e-14 Length: 1134  
 Score: 811.00 Matches: 151  
 Percent Similarity: 100.00% Conservative: 1  
 Best Local Similarity: 99.34% Mismatches: 0  
 Query Match: 28.46% Indels: 0  
 DB: 3 Gaps: 0

US-09-976-740-43 (1-538) x AAC59574 (1-1134)

QY 387 GlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValP  
 Db 921 CAGGGCCAGGATGAAGGGCGGGGGCAGCCCCGGGCGAGCGGACCCGCCAGGTGT  
 QY 407 MetAlaAlaMetAsnLysGluGlyThrAlaSerValAlaThrGlyProAsps  
 Db 861 ATGGCAGCCATGAACAAGGAAGGGGGAACAGCTTCTTTGCCACCGGGCCAGACT  
 QY 427 SerProValProLeuProGlyLysProAlaLeuProGlyValaAspGlyThrp  
 Db 801 TCCCGCTGCTTTGCCCGCCAGGCAACCCAGCCCTACTTGGGGCGGACGGGTCCC  
 QY 447 GlyCysProProGlyArgLysGluLysProSerAspProValGluTrpThrpValM  
 Db 741 GGCTGTCTCTCCCGGGCGCAAGAGAGCCATCGATCCCGTCGAGTGGAGCCGTGA  
 QY 467 ValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnG  
 Db 681 GTCTGCGAATATTTTACTGAGGCTGGATTCCCGAGAGCGGCGACAGCTTTCAG  
 QY 487 GluIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGlyL  
 Db 621 GAAATTGATGCAATCTTTGCTGCTCATGCGCGCACAGATGTGCTCACCAGCC  
 QY 507 IleArgLeuGlyProAlaLeuLysIleTyrGluHisIleValLeuGlnG  
 Db 561 ATCCGCTCGGGCCAGCCCTGAAATCTACGAACACCAATCAAGGTGCTTCAGC  
 QY 527 HisPheGluAspAspProAspGlyPheLeuGly 538  
 Db 501 CACTTTGAGGATGATGACCCCGATGCTTCTTAGGC 466

RESULT 12  
 ADB49888/c  
 ID ADB49888 standard; DNA; 460 BP.  
 XX  
 AC ADB49888;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO  
 XX toxic effect; gene expression profile; hepatotoxicity; diagnosti  
 KW toxicity marker; toxicity progression; drug screening;  
 KW Primary rat hepatocyte toxicity modelling; gene; ds.  
 OS Rattus norvegicus.  
 XX  
 PN WO2003065993-A2.  
 XX  
 PD 14-AUG-2003.  
 XX  
 PF 04-FEB-2003; 2003WO-US003482.  
 XX  
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 PR 10-APR-2002; 2002US-0371134P.  
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SUMMARIES

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91.8	12425	4	US-09-616-289-50		Sequence 50, Appl
91.0	2561	4	US-09-616-289-48		Sequence 48, Appl
51.1	1617	4	US-08-979-608A-11		Sequence 11, Appl
51.1	1617	4	US-09-517-849-11		Sequence 11, Appl
51.1	1617	4	US-09-616-289-11		Sequence 11, Appl
41.8	1422	4	US-08-979-608A-13		Sequence 13, Appl
41.8	1422	4	US-09-517-849-13		Sequence 13, Appl
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41.1	1208	4	US-08-979-608A-16		Sequence 16, Appl
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ALIGNMENTS

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; Sequence 45, Application US/09616289  
; Patent No. 6632923  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; APPLICANT: Arjona, Anibal A.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TRE  
; TITLE OF INVENTION: ATHEROSCLEROSIS  
; FILE REFERENCE: 10797-004001  
; CURRENT APPLICATION NUMBER: US/09/616,289  
; CURRENT FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/517,849  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: US 08/979,608  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: US 60/031,930  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 60/048,547  
; PRIOR FILING DATE: 1997-06-03  
; NUMBER OF SEQ ID NOS: 53  
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; SEQ ID NO 45  
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; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
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US-09-616-289-45  
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Pred. No.:



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plication US/09616289

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ION:

3, Ann M.

38, Robert S.

4, Simon W.

iona, Anibal A.

ION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

ION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

ION: ATHEROSCLEROSIS

: 10797-004001

ATION NUMBER: US/09/616,289

DATE: 2000-07-14

ION NUMBER: US 09/517,849

ATE: 2000-03-02

ION NUMBER: US 08/979,608

ATE: 1997-11-26

ION NUMBER: US 60/031,930

ATE: 1996-11-27

ION NUMBER: US 60/048,547

ATE: 1997-06-03

ID NOS: 53

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Qy  
497 nArgThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIle  
Db  
828 GCGCACCGATGTCCTCACCGGCTGTCCATCCGCTGGGGCCAGCGTTGAAATC

Qy  
517 uHisHisIleLysValLeuGlnGlnGlyHisPheGluAspAspAspProAspGly  
:::  
Db  
888 GCACCATATCAAGGTGCTGCAGCAGGGTCACTTCGAGGCGATGACCCGGAAAGC

Qy	537 uGly 538
Db	948 GGGa 951

RESULT 6  
US-09-616-289-11  
; Sequence 11, Application US/09616289

; GENERAL INFORMATION:  
 ; APPLICANT: Lees, Ann M.  
 ; APPLICANT: Lees, Robert S.

; APPLICANT: Arjona, Anibal A.

```

528 GGGCAGTGGCCACCGCCAGGTGTTCTCATGGCGGCGCTTGTAGTAAGGAGGGGG
QY aSerValAlaIaThrGlyProAspSerProSerProValProLeuProProGlyL
588 CTCTTCGACCACCGGGCTGACTTCCCGTCCCGGTGCTTTGCCCCCCCCGGGA
QY aLeuProGlyAlaAspGlyThrProPheGlyCysProProGlyArgLysGluL
648 CTTCCAGGAGCGATGGGACCCCTTTGGCTGCCCTGCCCGGGCGCAAGAGA
QY rAspProValGluTyrThrValMetAspValValGluTyrPheThrGluAlaG
708 AGACCCCGTGGATGGACAGTCATGGACGTCGTGGAGTACTTCCACGAGCGG
QY oGluGlnAlaThrAlaPheGlnGlnGluIleAspGlyLysSerLeuLeuL
768 TGGACCAAGCACCGCTTTCAGGAGCAGGAGATCGACCGCAAGTCCCTGCTG
QY nArgThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysI
828 GCGCACCGATGCTCTCACGGCGCTGTCCATCCGCTGGGGCCAGCGTTGAAA
QY uHisHisIleLysValLeuGlnGlnGlyHisPheGluAspAspAspProAspG
888 GCACCATATCAAGTGTCTGCAGCAGGTCACTTCGAGGACGATACCCCGGA
QY uGly 538
Db |||||
QY |||||
Db 948 GGG 951

RESULT 7
US-08-979-608A-13
; Sequence 13, Application US/08979608A
; Patent No. 6355451
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIA-
; TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,608A
; FILING DATE: 26-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,547
; FILING DATE: 03-JUN-1997
; APPLICATION NUMBER: US 60/031,930
; FILING DATE: 27-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/5)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1422 base pairs

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E: nucleic acid  
 ANDEDNESS: single  
 OLOGY: linear  
 E/KEY: Coding Sequence  
 ATION: 1...756  
 DESCRIPTION: SEQ ID NO: 13:

1.35e-37 Length: 1422  
 1191.50 Matches: 223  
 Y: 95.24% Conservative: 17  
 ity: 88.49% Mismatches: 9  
 Indels: 3  
 Gaps: 2  
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(1-538) x US-08-979-608A-13 (1-1422)

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 SerAlaArgProSerArgSerLysArgGlyGlyGluGluArgValLeuGluLysGlu 329  
 AGCGCCCGCGCGCGCGGACACAGAGAGCTGGCGAGGAGCGAGTGTGTAAGAGGAG 120  
 GluGluAspAspAspGluAspGluAspGluAspGluAspGluAspGluAspGlu 347  
 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
 GluValProGluSerArgProAlaGlyAlaGlnHisHisGlnLeuAsn---Gly 366  
 GAGGTGCCGAGAGCGATCGTCCCGGGGTGGCGAGCATCACAGCTGAATGGCGGC 240  
 ArgGlyProGlnSerAlaLysGluArgValLysGluThrProCysGlyProHis 386  
 CGCGCGCGCGAGCG 300  
 GlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValPheSer 406  
 GGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 AlaAlaMetAsnLysGluGlyGlyThrAlaSerValAlaThrGlyProAspSerPro 426  
 GCGGCTTTAGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
 ProValProLeuProProGlyLysProAlaLeuProGlyAlaAspGlyThrProPhe 446  
 CCGGTGCTTTGCG 480  
 CysProProGlyArgLysGluLysProSerAspProValGluThrThrValMetAsp 466  
 TGCCCTGCG 540  
 ValGluThrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGluGln 486  
 GTGGAGTACTTACCGAGCGCGGCTTCCCTGAGCAAGCCACCGGCTTTCCAGAGCAG 600  
 IleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSer 506  
 ATCGAGCGCAAGTCTGCTGCTCATGACGCGCACCGGATGCTCTCACCGGCGTGTCC 660  
 ArgLeuGlyProAlaLeuLysLysLysGluHisHisLysLysValLeuGlnGlnGly 526  
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 PheGluAspAspAspProAspGlyPheLeuGly 538  
 TTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 756

Sequence 13, Application US/09517849  
 Patent No. 6605588  
 GENERAL INFORMATION:  
 APPLICANT: Lees, Ann M.  
 Law, Robert S.  
 Arjona, Anibal A.  
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
 BINDING PROTEINS AND THEIR USES IN DIAG  
 TREATING ATHEROSCLEROSIS  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/517,849  
 FILING DATE: 02-Mar-2000  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/979,608  
 FILING DATE: 26-NOV-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Myers, Louis  
 REGISTRATION NUMBER: 35,965  
 REFERENCE/DOCKET NUMBER: 10797-003001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1422 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: Coding Sequence  
 LOCATION: 1...756  
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 US-09-517-849-13

Alignment Scores:  
 Pred. No.: 1.35e-37 Length: 1422  
 Score: 1191.50 Matches: 223  
 Percent Similarity: 95.24% Conservative: 17  
 Best Local Similarity: 88.49% Mismatches: 9  
 Query Match: 41.81% Indels: 3  
 DB: 4 Gaps: 2  
 US-09-976-740-43 (1-538) x US-09-517-849-13 (1-1422)  
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 Db 1 ACCGCTCTCGAGCGCTTGGCTGCCCGCGGGACAGCGCCGCGCGCCACCGGCCAC  
 Qy 310 AlaSerAlaArgProSerArgSerLysArgGlyGlyGluGluArgValLeuGlu  
 Db 61 GCCAGCGCCCGCGCGCGGACACAGAGAGCTGGCGAGGAGCGAGTGTGTAAG  
 Qy 330 GluGluAspAspAspGluAspGluAspGluAspGluAspGluAspGluAsp  
 Db 121 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
 Qy 348 SerGluValProGluSerArgProAlaGlyAlaGlnHisHisGlnLeuAsn  
 Db 181 TCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG







Law, Simon W.  
 Arjona, Anibal A.  
 INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
 BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
 TREATING ATHEROSCLEROSIS

SEQUENCES: 42  
 NDNCE ADDRESS:  
 RESSEE: Fish & Richardson P.C.  
 SER: 225 Franklin Street  
 Y: Boston  
 IE: MA  
 TRY: USA  
 : 02110-2804

READABLE FORM:  
 IUM TYPE: Diskette  
 PUTER: IBM Compatible  
 RATING SYSTEM: DOS  
 IWARE: FastSeq for Windows Version 2.0

APPLICATION DATA:  
 LICATION NUMBER: US/08/979,608A  
 ING DATE: 26-Nov-1997

PLICATION DATA:  
 LICATION NUMBER: US 60/048,547  
 ING DATE: 03-JUN-1997  
 LICATION NUMBER: US 60/031,930  
 ING DATE: 27-NOV-1996

AGENT INFORMATION:  
 3: Myers, Louis

ISTRATION NUMBER: 35,965  
 RENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

INATION INFORMATION:  
 3PHONE: 617/542-5070  
 3EAX: 617/542-8906  
 OR SEQ ID NO: 12:

CHARACTERISTICS:  
 3TH: 1362 base pairs  
 3: nucleic acid  
 ANEDNESS: single  
 OLOGY: linear

3/KEY: Coding Sequence  
 ATION: 1...696  
 DESCRIPTION: SEQ ID NO: 12:

1.15e-33	Length:	1362
1086.50	Matches:	203
94.83%	Conservative:	17
87.50%	Mismatches:	9
38.12%	Indels:	3
4	Gaps:	2

(1-538) x US-08-979-608A-12 (1-1362)

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 GluLysAspAspGluAspGluAspGluAspAsp-----ValSerGluGly 347  
 |||||  
 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
 |||||  
 GluValProLysSerArgProAlaGlnHisGlnHisGlnLeuAsn---Gly 366  
 GAGGTGCCGAGAGCGATCGTCCCGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAG 180  
 |||||  
 ArgGlyProGlnSerAlaLysGluArgValLysGluThrProCysGlyProHis 386  
 |||||  
 CGCGGCGCGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240  
 |||||  
 GlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnValPheSer 406  
 |||||

241 CCTGCGCAGGAGGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGT  
 QY MetAlaAlaMetAsnLysGluGlyThrAlaSerValAlaThrGlyProAsps  
 |||||  
 301 ATGGCGGCGCTTGGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT  
 Db ATGGCGGCGCTTGGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT  
 |||||  
 427 SerProValProLeuProGlyLysProAlaLeuProGlyValaAspGlyThrP  
 QY |||||  
 361 TCCCGCGTGCCTTGGCCCCCGGGAAGCAGCCCTCCAGAGGAGCGATGGGACCC  
 Db |||||  
 447 GlyCysProProGlyArgLysGluLysProSerAspProValGluThrValM  
 QY |||||  
 421 GCGTGCCTCGCGCGCAAGAGAGAGCGCGGAGAGCGCGCGCGCGCGCGCGCGTCA  
 Db |||||  
 467 ValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnG  
 QY |||||  
 481 GTGCTGGAGTACTTACCGAGGCGGCGCTTCCCTGAGCAAGCCAGCGCTTCCAGG  
 Db |||||  
 487 GluIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGlyL  
 QY |||||  
 541 GAGATCGACGCGCAAGTCCCTGCTGCTCATGCGAGCGCAGCGATGCTCCTCACC  
 Db |||||  
 507 IleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnG  
 QY |||||  
 601 ATCCGCGCTGGGCGCGCGTGTGAAATCTATGAGCACCATATCAAGGTGCTGCAGC  
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 527 HisPheGluAspAspProAspGlyPheLeuGly 538  
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 661 CACTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 696  
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RESULT 14  
 US-09-517-849-12  
 : Sequence 12, Application US/09517849  
 : Patent No. 6605508  
 : GENERAL INFORMATION:  
 : APPLICANT: Lees, Ann M.  
 : Law, Simon W.  
 : Arjona, Anibal A.  
 : TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
 : BINDING PROTEINS AND THEIR USES IN DIAGN  
 : TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/517,849  
 FILING DATE: 02-Mar-2000  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/979,608  
 FILING DATE: 26-NOV-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Myers, Louis  
 REGISTRATION NUMBER: 35,965  
 REFERENCE/DOCKET NUMBER: 10797-003001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1362 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single

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: ME/KEY: Coding Sequence
:
: TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
:
: TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TR
:
: TITLE OF INVENTION: ATHEROSCLEROSIS
:
: FILE REFERENCE: 10797-004001
:
E DESCRIPTION: SEQ ID NO: 12:

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? PRIOR APPLICATION NUMBER: US 09/511,849  
 ? PRIOR FILING DATE: 2000-03-02  
 ? PRIOR APPLICATION NUMBER: US 08/979,608  
 ? PRIOR FILING DATE: 1997-11-26  
 ? PRIOR APPLICATION NUMBER: US 60/031,930  
 ? PRIOR FILING DATE: 1996-11-27  
 ? PRIOR APPLICATION NUMBER: US 60/048,547  
 ? PRIOR FILING DATE: 1997-06-03  
 ? NUMBER OF SEQ ID NOS: 53  
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; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1362

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; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
; SEQ ID NO 12
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (696)
US-09-616-289-12

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; ORGANISM: Oryctolagus cuniculus
;
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: (1)...(696)
US-09-616-289-12

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US-09-616-289-12	
Alignment Scores:	
Pred. No.:	1.15e-33
Score:	1086.50
Percent Similarity:	94.83%
Best Local Similarity:	87.50%
Query Match:	38.12%
Length:	1362
Matches:	203
Conservative:	17
Mismatches:	9
Indels:	3

Score:	1086.50	Matches:	203
Percent Similarity:	94.83%	Conservative:	17
Best Local Similarity:	87.50%	Mismatches:	9
Query Match:	38.12%	Indels:	
DB:	4	Gaps:	2
US-09-976-740-43 (1-538) x US-09-616-289-12 (1-1362)			

[illegible]

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      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

330 GluGluGluAspAspClnAspGluAspGluGluAspAsp-----ValSer
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	:	:	:
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Qy	
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Db	
367	GluArgGlyProGlnSerAlaLysGluArgValLysGluTrpThrProCysGln
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DB	181	GAGCGGGCCCGCAGACCCCAAGGAGCGGGCCAGGAGTGGTCGCTGTGTGGG
QY	387	GinGlyGinAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnVal
DB	241	CCTGGCCAGGAGGAGGGCGGGCGCGCGGGCAGTGGCCACCCGCCAGGTC
QY	407	MetAlaAlaMetAsnLysGluGlyThrAlaSerValAlaThrGlyProAsp

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407	MetAlaAlaMetAsnLysGluGlyGlyThrAlaSerValaIaThrGlyProAsi	QY
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361	TCCCGGGTGCCCTTCGCCCCCCGGGAAGCCAGACCTCCCAAGGAGCCGATGGAGCC	Db
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361	TCCCGGTCCTTTGCCCGCCGGGAAGCAGCCCTCCGAGGACCGATGGGAC	Db
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467	ValValGluTrpPheThrGluAlaGlyPheProGluAlaThrAlaPheGlu	W

[illegible]

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09:28:16 2004

us-09-976-740-43.rni

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March 13, 2004, 04:07:02  
6 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using frame\_plus\_p2n model

March 12, 2004, 20:46:42 ; Search time 778.355 Seconds  
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2544.725 Million cell updates/sec

US-09-976-740-43

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BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

2432557 seqs, 1840798884 residues

hits satisfying chosen parameters: 4865114

length: 0  
length: 2000000000

Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Published Applications NA:

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is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

#### SUMMARIES

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4	2850	100.0	1614	1614	13	US-10-023-523-45	Sequen
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7	2616.5	91.8	12425	12425	12	US-10-671-242-50	Sequen
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10	2616.5	91.8	12425	12425	15	US-10-616-187-50	Sequen
11	2594	91.0	2561	2561	9	US-09-976-740-48	Sequen
12	2594	91.0	2561	2561	12	US-10-671-242-48	Sequen
13	2594	91.0	2561	2561	13	US-10-023-529-48	Sequen
14	2594	91.0	2561	2561	13	US-10-023-523-48	Sequen
15	2594	91.0	2561	2561	15	US-10-616-187-48	Sequen
16	1470	51.6	1445	1445	10	US-09-945-527-6	Sequen
17	1455.5	51.1	1617	1617	9	US-09-962-055-11	Sequen
18	1455.5	51.1	1617	1617	9	US-09-976-740-11	Sequen
19	1455.5	51.1	1617	1617	12	US-10-671-242-11	Sequen
20	1455.5	51.1	1617	1617	13	US-10-023-529-11	Sequen
21	1455.5	51.1	1617	1617	13	US-10-023-523-11	Sequen
22	1455.5	51.1	1617	1617	15	US-10-616-187-11	Sequen
23	1260	41.2	1336	1336	14	US-10-102-806-247	Sequen
24	1191.5	41.8	1422	1422	9	US-09-962-055-13	Sequen
25	1191.5	41.8	1422	1422	9	US-09-976-740-13	Sequen
26	1191.5	41.8	1422	1422	12	US-10-671-242-13	Sequen
27	1191.5	41.8	1422	1422	13	US-10-023-529-13	Sequen
28	1191.5	41.8	1422	1422	13	US-10-023-523-13	Sequen
29	1191.5	41.8	1422	1422	15	US-10-616-187-13	Sequen
30	1170	41.1	1208	1208	9	US-09-962-055-16	Sequen
31	1170	41.1	1208	1208	9	US-09-976-740-16	Sequen
32	1170	41.1	1208	1208	12	US-10-671-242-16	Sequen
33	1170	41.1	1208	1208	13	US-10-023-529-16	Sequen
34	1170	41.1	1208	1208	13	US-10-023-523-16	Sequen
35	1170	41.1	1208	1208	15	US-10-616-187-16	Sequen
36	1086.5	38.1	1362	1362	9	US-09-962-055-12	Sequen
37	1086.5	38.1	1362	1362	9	US-09-976-740-12	Sequen
38	1086.5	38.1	1362	1362	12	US-10-671-242-12	Sequen
39	1086.5	38.1	1362	1362	13	US-10-023-529-12	Sequen
40	1086.5	38.1	1362	1362	13	US-10-023-523-12	Sequen
41	1086.5	38.1	1362	1362	15	US-10-616-187-12	Sequen
42	402	14.1	2307	2307	10	US-09-893-519A-87	Sequen
C 43	391	13.7	3331	3331	11	US-09-373-658-31	Sequen
C 44	391	13.7	3331	3331	11	US-09-989-687-31	Sequen
C 45	366	13.5	1926	1926	14	US-10-294-804-3	Sequen

#### ALIGNMENTS

RESULT 1  
US-09-976-740-45  
; Sequence 45, Application US/09976740  
; Publication No. US20020194633A1  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; APPLICANT: Arjona, Anibal A.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TRE  
; FILE REFERENCE: 10797-004001  
; CURRENT APPLICATION NUMBER: US/09/976,740  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 09/616,289  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/979,608  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: US 60/031,930  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 60/048,547  
; PRIOR FILING DATE: 1997-06-03  
; NUMBER OF SEQ ID NOS: 53

3EQ for Windows Version 4.0

3 sapiens

... (1614)

5.74e-144	Length:	1614
2850.00	Matches:	538
100.00%	Conservative:	0
100.00%	Mismatches:	0
100.00%	Indels:	0
9	Gaps:	0

(1-538) x US-09-976-740-45 (1-1614)

AlaGlyProProAlaLeuProProGluThrAlaAlaAlaThrThrAlaAla 20  
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AlaSerSerAlaAlaSerProHisTyrGlnGluTrrIleLeuAspThrIleAsp 40  
3CTCGTCGTCGGCGCTTCCCGGCATCCAAAGAGTGGATCTCGACACCATCGAC 120  
LeuArgSerArgLysAlaAArgProAspLeuGluArgIleCysArgMetValArgArg 60  
TTCGGCTCGCGCAAGGCGGGCGCGACCTGGAGCGCATCTGCCGATGTGTGGCGG 180  
HisGlyProGlnProGluArgThrArgAlaGluLeuGluLysLeuIleGlnArg 80  
TACGGCCCGGAGCGCGAGCGACGCGCGCGAGTCTCGAGAACTGATCAGCAGCGC 240  
ValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAaArgValGln 100  
3TGCTCGGGTCAGTACAAAGGGAGCATCTGTCACCGAACGCGGGCGCGCTCCAG 300  
ProArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyAlaProAla 120  
TCCGGGGCGGAGCACCCCGCGCGCCGCGCGCGCCCCCGCGGGCGCCCCCGCC 360  
AlaAlaAlaAlaAlaProProProThrProAlaProProProProProAlaProAla 140  
3CGCGCGCGCGCGCGCGCGCCCGACGCGCGCGCCCGCGCGCCACCGCGCGCGCCGTC 420  
AlaAlaAlaProAlaArgAlaProArgAlaAlaAlaAlaAlaThrAlaProPro 160  
3CGCGCGCCCCGGCGCGGGCGCCCGCGCGCGCGCGCGCGCCACAGCGGCGCCCCC 480  
ProGlyProAlaGlnProGlyProArgAlaGlnArgAlaAlaProLeuAlaAlaPro 180  
TCTGGCCCCCGCAGCGCGGGCCCCCGCGCGCAGCGGGCGCGCGCCCTGGCGCGCGCG 540  
ProAlaProAlaAlaProAlaValAlaProProAlaGlyProArgArgAlaPro 200  
TCCGCGCGCAGCGCTCCCGCGCGGGTGGCGCGCCCGCGCGCGCGCGCGCGCCCCC 600  
ProAlaValAlaAlaArgGluProProLeuProProProGlnProProAlaPro 220  
TCCGCGCTCGCCCGCCCGGGAGCGCGCTGCCCGCGCGCGCCACAGCGCGCGCGCGCG 660  
3IleGlnGlnProProProProGlnProGlnProProProProGluGlyGlyAlaVal 240  
TACGAGCAGCAGCGCGCGCGCGCGCAGCGCCACAGCGCGCGCGCGGAGGGGGCGCGGTG 720  
AlaGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrLeuGlyGly 260  
3CGCGCGCGCGCGCGCGCGCGTGGAGCTCGGGGAAGTCGTGCGCTACTCGCGGGGGC 780  
3IlyGlyAlaGlyArgLeuThrArgGlyArgValGlnGlyLeuLeuGluGluGlu 280

781	AGCGCGCGCGCGCGGCTGCCTTAACCGCGCGCGCGCTGCAGGGGCTGCCTGGAG	Db
281	AlaAlaIleArgGlyArgLeuGluArgThrArgLeuGlyAlaLeuAlaLeuProA	Qy
841	GGCGGGCTCGAGGCGGCTCGAGAGCGCACCGCTCTCGAGGCGCTTGCGCTGCCCC	Db
301	AspArgProGlyArgAlaProProAlaAlaSerAlaArgProSerArgSerLysA	Qy
901	GAAGCCCGGAGCGGGCGCGCGCGCGCCAGCGCCCGCTCTCGACGCAAGA	Db
321	GlyGluGluArgValLeuGluLysGluGluGluAspAspGluAspGluA	Qy
961	GGAGAGAGCGAGTACTTGAGAAAGAGAGAGAGATGATGATGAAGATGAAG	Db
341	GluAspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyA	Qy
1021	GAAGATGATGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCTCTGCGGTG	Db
361	HisHisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysG	Qy
1081	CACCACCACAGCTTAACGGCGAGCGGGGACCTCAGAGTGCCCAAGGAGAGGGTCAAAG	Db
381	ThrProCysGlyProHisGlnGlyIleAspGluGlyArgGlyProAlaProGlyLys	Qy
1141	ACCCCTTCGGGACCGCACACAGGGCGAGATGAAGGGCGGGGGCCAGCCCGCGGCA	Db
401	ThrArgGlnValPheSerMetAlaAlaMetAsnLysGlyGlyThrAlaSerV	Qy
1201	ACCCGCCAGGTGTTCTCCATGCGCAGCCATGAACAAGGAAAGGGGGAACAGCTTCTG	Db
421	ThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuP	Qy
1261	ACCGGGCCAGACTTCGCCGCTGCCCGCTGCTTTGCCCCCAGGCAAAACGAGCCCTAC	Db
441	AlaAspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAspP	Qy
1321	GCCGACGGGACCCCTTTGGCTGTGCCCGCGGGCGCAAGAGAACCATCTGATC	Db
461	GluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGluG	Qy
1381	GAGTGGACCGTGATGTGCTGAATATTTTACTGAGGCTCGATTCCCGGAGC	Db
481	ThrAlaPheGlnGluGlnIleAspGlyLysSerLeuLeuLeuMetGlnArgT	Qy
1441	ACAGCTTTCCAAAGACAGCAAAATTTGATGGCAATCTTTTGCTGCTCATGCAGGGCA	Db
501	ValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisH	Qy
1501	GTGCTCACCGGCTGTCCATCCGCGCTCGGGCGAGCCCTGAAATCATCTACGAGCACCC	Db
521	LysValLeuGlnGlnGlyHisPheGluAspAspProAspGlyPheLeuGly	Qy
1561	AAGGTGCTTCAGCAAGGCCACTTTGACGATGATGACCCCGATCGCTTCTTAGGC	Db

## RESULT 2

RESOLUTION 2  
US-10-671-242-45  
Sequence 45, Application US/10671242  
Publication NO. US20040040049A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: PROTEIN LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/671,242  
CURRENT FILING DATE: 2003-09-24  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849

DATE: 2000-03-02  
 ATION NUMBER: US 08/979,608  
 DATE: 1997-11-26  
 ATION NUMBER: US 60/031,930  
 DATE: 1996-11-27  
 ATION NUMBER: US 60/048,547  
 DATE: 1997-06-03

2.13 NOS: 33  
tSEQ for Windows Version 4.0

mo sapiens

15) ... (1674)

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3:      5.74e-144      Length:      1614
      2850      Matches:      538
      100.00%      Conservative:      0
      100.00%      Mismatches:      0
      100.00%      Indels:      0
      12      Gaps:      0

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(1-538) x US-10-671-242-45 (1-1614)

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aAlaSerSerAlaAlaSerProHisTyrGlnGluTyrIleLeuAspThrIleAsp 40  
CGCTCGTGTGTCGCGCGCTTCCCGCGACTACCAAGAGTGGATCTGGACACATCGAC 120  
rLeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetValArgArg 60  
GCTGCGCTCGCGCAAGCGGGCGCGGACCTCGGAGCGCATCTGCGGATGTTGGCGGG 180  
gHisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGlnArg 80  
GCACGCGCCGGAGCCCGAGCGCACCGCGCGAGCTCGAGAACTGATCAGACGCGC 240  
aValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgValGln 100  
CGTGCTCCGGGTGAGTACAAAGGGAGCATCTCGTACCGCAACGCGCGCGTCCAG 300  
oProArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyAlaProAla 120  
CCCCGGCGGGAGCCACCCTCGCGCCCGCGCGCGCCCCCGGGCGCCCGCGCC 360  
aAlaAlaAlaAlaProProProThrProAlaProProProProAlaProVal 140  
CGCGCGCGCGCGCGCGCGCGCCACGCGCGCCCGCGCGCCCGCGCGCGCGCCGTC 420  
aAlaAlaProAlaArgAlaProArgAlaAlaAlaAlaAlaThrAlaProPro 160  
CGCC 480  
cProGlyProAlaGlnProGlyProArgAlaGlnArgAlaAlaProLeuAlaAlaPro 180  
CGCTGGCCCCCGCGACGCGGGCCCCCGCGGCGAGCGGGCGCGCCCTGGCGCGCGCG 540  
oProAlaProAlaAlaProProAlaValAlaProProAlaGlyProArgArgAlaPro 200  
CGCGCGCGCAGCGCGCTCCCGCGCGTGGCGCCCCCGCGCGCGCGCGCGCGCCCC 600  
oProAlaValAlaAlaArgGluProProLeuProProProProGlnProProAlaPro 220  
CGCGCGCTGCGCGCCCGGAGCGCGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
GlnGlnGlnGlnProProProProGlnProGlnProProProGlnGlyGlyValVal 240

661	DB	CCACAGCAGCAGCAGCCGCCGCCGCCGCCAGCCACAGCCGCCGCCGCCAGAGGGGG
241	QY	ArgAlaGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrLe
721	DB	CGGGCCGGCGCGCGCGGCCCGTGAGCCTCGCGGAGTCTGTCGCCCTACCT
261	QY	SerGlyGlyAlaGlyGlyArgLeuThrArgGlyArgValGlnGlyLeuLeuGly
781	DB	AGCCGCGCGCGCGCGCGCTCGCCTAACCCGCGCGCGCTGCAGGGCGCTGTGA
281	QY	AlaAlaAlaArgGlyArgLeuGluAlaArgThrArgLeuGlyAlaLeuAlaLeuPr
841	DB	CGCGCGCTCGAGGCGCTGTGGAGCGCACCCGCTCTCGAGCGCTTGCCTGCC
301	QY	AspArgProGlyArgAlaProProAlaAlaSerAlaAlaArgProSerArgSerLy
901	DB	GACAGGCCCGAGCGGGCGCCCGCGCGCCGAGCGCCGCCCGCTCTCGACGAA
321	QY	GlyGluGluArgValLeuGluLysGluGluGluGluAspAspGluAspGly
961	DB	GGAGAGAGCGAGTACTTGGAGAGAGAGAGAGAGAGATGATGATGAAGATGA
341	QY	GluAspAspValSerGluGlySerGluValProGluSerAspArgProAlaGly
1021	DB	GAAGATGATGTCTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCCTCTCGAGG
361	QY	HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLys
1081	DB	CACCACCAGCTTAACCGCGAGCGGGACCTCAGATGTCCAAGGAGAGGGTCAAC
381	QY	ThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly
1141	DB	ACCCCTTCCGGACCGCACAGGGCCAGAGATGAAGGGCGGGGCGCACGCCCGGG
401	QY	ThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer
1201	DB	ACCCGCCAGGTGTTCTCCATGGCAGCCATGAACAAGAGAGGGGGAACAGCTTC
421	QY	ThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu
1261	DB	ACCGGGCCAGACTCCCCCGTCCCCCGTGCCCTTTGCCCCACAGGCAAAACAGCCCTT
441	QY	AlaAspGlyThrProPheGlyCysProProGlyArgLysGluLysProSerAsp
1321	DB	GCCGACGGAGACCCCTTTGGCTGTCCGCCCGGGCGCAAGAGAGCCATCTTGAT
461	QY	GluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGly
1381	DB	GAGTGGACCGTGATGATGTCGCAATATTTTACTGAGCGTGGATTTCCCGAG
481	QY	ThrAlaPheGlnGluGlnGluLeuAspGlyLysSerLeuLeuLeuMetGlnArg
1441	DB	ACAGCTTTCCAGAGCAGGAATTTGATGGCAATCTTTTGCTGCTCATGCGAGCGC
501	QY	ValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis
1501	DB	GTGCTCACCGGCTGTTCATCCGCTCGGGCCAGCCCTGAAATCTACGAGCAC
521	QY	LysValLeuGlnGlnGlyHisPheGluAspAspProAspGlyPheLeuGly
1561	DB	AAGGTGCTTCACAAAGGCCATTTTGAGATGATGACCCCGATGGTCTTTAGGC

## RESULT 3

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US-10-023-529-45
; Sequence 45, Application US/10023529
; Publication No. US2002012938A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

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GTGGACCGTGATGGATCGTCGAATATTTTACTGAGGCTGGATTCCCGGACAGGCG 1440  
 rAlaPheGlnGluGlnGluLeuAspGlyysSerLeuLeuMetGlnArgThrAsp 500  
 AGCTTTCCAGAGCAGGAAATGATGGCAATCTTTTGTGCTCATGAGGCGCACAGAT 1500  
 uLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuysIleTyrGluHisIle 520  
 GCTACCGCGCTGTCTCATCGGCTCGGGCCAGCCCTGAAATCTACGAGCACCATC 1560  
 sValLeuGlnGlnGlyHisPheGluAspAspProAspGlyPheLeuGly 538  
 GGTGCTTCAGCAGGCGCACTTGTAGAGATGATGACCCCGATGCTTCITAGGC 1614

Application US/09976740

US20020194633A1

ATION:

es, Ann M.

es, Robert S.

aw, Simon W.

rjona, Anibal A.

NTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

NTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

NTION: ATHEROSCLEROSIS

E: 10797-004001

CATION NUMBER: US/09/976,740

G DATE: 2001-10-12

TION NUMBER: 09/616,289

DATE: 2000-07-14

TION NUMBER: US 08/979,608

DATE: 1997-11-26

TION NUMBER: US 60/031,930

DATE: 1996-11-27

TION NUMBER: US 60/048,547

DATE: 1997-06-03

ID NOS: 53

tSEQ for Windows Version 4.0

5

no sapiens

6.82e-131 Length: 12425  
 2616.50 Matches: 536  
 Y: 69.16% Conservative: 0  
 irity: 69.16% Mismatches: 2  
 91.81% Indels: 239  
 9 Gaps: 4

(1-538) x US-09-976-740-50 (1-12425)

AlaGlyProProAlaLeuProProGluThrAlaAlaAlaAlaThrThrAlaAla 20  
 XCGGGGCCCCCGGCGCTTACCCCGCGGAGACGGCGCGCGCGCCACCGCGGCG 2891  
 AlaSerSerAlaAlaSerProHisTyrGlnGluTyrPileLeuAspThrIleAsp 40  
 XGCTCGTCCGCGCGCTTCCCGCACCTACCAAGAGTGGATCTCGACACCATCGAC 2951  
 LeuArgSerArgJyAlaArgProAspLeuGluArgIleCysArgMetValArgArg 60  
 XCTGCGCTCGCGCAAGCGCGCGGACCTGAGAGCGCATCTGCCGATGTTGGCGGG 3011  
 HisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGlnArg 80  
 XACGCGCGCGGAGCGGAGCGCACGCGCGCGAGCTCGAGAACTGATCCAGCAGGCG 3071  
 ValLeuArgValSerTyrTysGlySerIleSerTyrArgAsnAlaAlaArgValGln 100

3072 GCCTGTCTCCGGGTACGTACAGGGGAGCATCTCTGTACCGCAACGCGGCGG 101 ProProArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyAl 3132 CCGCCCGCGCGGAGCACCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGG 121 AlaAlaAlaAlaAlaProProProThrProAlaProProProProProAl 3192 GCGG 141 AlaAlaAlaAlaProAlaArgAlaProArgAlaAlaAlaAlaAlaThrAl 3252 GCAG 161 SerProGlyProAlaGlnProGlyProArgAlaGlnArgAlaAlaProLeuAl 3312 TCCTCTGGCGG 181 ProProAlaProAlaAlaProProAlaValAlaProProAlaGlyProArgAl 3372 CCGCGCGCGCGCGCGCTCCCGCGCGGTGGCGCGCGCGCGCGCGCGCGCGG 201 ProProAlaValAlaAlaArgGluProProLeuProProProProProPro 3432 CCGCGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 221 ProGlnGlnGlnProProProProGlnProGlnProProProProGlnGly 3492 CCACAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 241 ArgAlaGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrLe 3552 CCG 261 SerGlyGlyAlaGlyGlyArgLeuThrArgGlyArgValGlnGlyLeuLeu 3612 AGCGG 281 AlaAlaAlaArgGlyArgLeuGluArgThrArgLeuGlyAlaLeuAlaLeu 3672 GCGCGCGCTCGAGGCGCTCTGGAGCGCACCCGCTCTGGAGCGCTTGGCTGCC 301 AspArgProGlyArgAlaProProAlaAlaAlaSerAlaArgProSerArg 3732 GACAGGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 316 ----- 3792 GCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTTGGTGGC 316 ----- 3852 GCGAGTCCCGGAGGAACTGGGTGGCGGCTGGCTGGGGCTTTTGGCGCGGTTTCC 316 ----- 3912 CTCGTGGTGGTGACCTTGGCAAGTGATTGAATCTCCCGCGGCGCTCAGTTTCC 316 ----- 3972 GTAAACGCGGTTTAATAACAGTAGCGACCCCTTGGGGTGTGTGAGCGAGTTTAG 316 ----- 4032 TTGGTTGTGAGGCGTTTAGTTAAACAGAGCGCTGGCAGCGAGTGAATGCGTAA 316 ----- 4092 GTCGCTATTGTTCTTAAAGTGAATCGTTTCTCTCTCCCGCGCGGAGCGC 317 ----- Ser 4152 CAGGCTCTGGGATTAGAACAGCTACTAATTTTGTGATCTTCTCTCTCGGCTCC



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QY      416 -----
Db      4511 CCCTCGGTTGGGAAGAGTGCTAGGTGGAGAGGAACCTCAGCCCGAAGACAA
QY      417 -----AlaSerValAlaThrGlyProAspSerProS
Db      4571 ACAGTGTTTTTTTCCCTTCCAGCTTCTGTGTGCCACCGGGCCAGACTCCCGGT
QY      429 lProLeuProGlyLysProAlaLeuProGlyValaAspGlyThrProPheG
Db      4631 GCCTTTGCCCCCGACGCAACCAAGCCCTACTCTGGGGCCGACGGACCCCTTTTG
QY      449 o-----
Db      4691 GTAAGTTGGGGTATTGAGACATGGGGGTGCTGCTCAGGTGTGTGTTACAGCGC
QY      450 -----ProGlyArgLysGluI
Db      4751 CATCCGTGTTCACTGGTGTCTGTTTGTGTGATGCAGTCCCGGGCGCAAGAGF
QY      457 erAspProValGluTyrThrValMetAspValValGluTyrPheThrGluAlaC
Db      4811 CTGATCCGTCGATGGACCGTGATGGATGTCGTGCAATATTTTACTGAGGCTC
QY      477 roGluInAlaThrAlaPheGlnGlu-----
Db      4871 CGGAGCAGGCGACAGCTTTCCAAGA- GCAGGTGAGTTTCCAGCCCGAGGACTACA
QY      485 -----
Db      4930 CAGACACAGAGGCGCTCCCTGGGATGTGCGCTGATCCCGGGTTTCTGTGTCTCT
QY      486 --GlnGluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuT
Db      4990 CCCAGGAATTGATGCAAACTTTTGTCTCATCGACGGCACATGTGCTCA
QY      505 euSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisIleLysValL
Db      5050 TGTCCATCCGCTCGGGCGAGCCCTGAAAACTACGAGCACCACATCAAGGTGC
QY      525 lngLysHisPheGluAspAspProAspGlyPheLeuGly 538
Db      5110 AAGGCCACTTTGAGGATGATGACCCCGATGCTTCTTAGGC 5150

RESULT 8
US-10-023-529-50
; Sequence 50, Application US/10023529
; Publication No. US20020129388A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TRE
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,529
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO. 50

```

o sapiens

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6.82e-131      Length:      12425
2616.50        Matches:      536
V: 69.16%      Conservative: 0
ity: 69.16%    Mismatches:  2
91.81%         Indels:      239
13             Gaps:         4

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(1-538) x US-10-023-529-50 (1-12425)

AlaGlyProProAlaLeuProProGluThrAlaAlaAlaThrAlaAa 20  
 GCGGGGCCCGGGCTTACCCGCCGAGACGCGCGCGCCGACCCACGCGGGCC 2891  
 AlaSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIleAsp 40  
 GCCTGTCGTCCGCGCGCTTCCCGGCACTTACCAGAGTGGATCTCTGGACACATCGAC 2951  
 LeuArgSerArgLyAlaArgProAspLeuGluArgIleCysArgMetValArgArg 60  
 CTGCGCTCGCGCAAGCGCGCGCCGACCTTGGAGCGCATCTGCCGGAATGGTGGCGCG 3011  
 HisGlyProGluProGluArgThrArgAlaGlnLeuGluIysLeuIleGlnGlnArg 80  
 CACGGCCCGAGCGGAGCGCACGCGCGCGAGCTCGAGAAACTGATCTCACGACGCGC 3071  
 ValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgValGln 100  
 TTGCTTCGGGTGAGCTTACAGGGGAGCATCTCTGTACCGCAACGCGCGCGCTCCAG 3131  
 ProArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyAlaProAla 120  
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 AlaAlaAlaAlaProProProThrProAlaProProProProProAlaProVal 140  
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 CG 3311  
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 CG 3431  
 ProAlaValAlaAlaArgGluProProLeuProProProProGlnProProAlaPro 220  
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 HisGlnGlnProProProProGlnProGlnProProProGluGlyGlyAlaVal 240  
 TAGACACAGCGCGCGCGCGCGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCG 3551  
 AlaGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrLeuGlyGly 260  
 CG 3611  
 HisGlyAlaGlyGlyArgLeuThrArgGlyArgValGlnGlyLeuLeuGluGlu 280  
 CG 3671  
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D	b	3672	GCGCGCGCTCGAGGCGGTCTGGAGCGCACCGGCTCTCGAGAGCGCTTGGCGTGCCGC
Q	y	301	AspArgProGlyArgAlaProProAlaIalaSerAlaIargProSerArg- 
D	b	3732	GACAGCCCCGAGCGGGCGGCCGCCAGCGCCCGCCGTCGTCAGCAAGC 
Q	y	316	- - - - -
D	b	3792	GCGCCGGGAGCGGGGCGCGCGGTGGCAGGTGCGGCGAAGTTGTGTGGGC
Q	y	316	- - - - -
D	b	3852	GCGAGTCCGGAGGAACCTGGGTGGCGGTGGCTGGGGCTTTTGGCGCGTTTCT
Q	y	316	- - - - -
D	b	3912	CTCGGTGCGTGTGACCTTGGCAAGTGATTGAATCTCCCAGAGCCTCAGTTTCT
Q	y	316	- - - - -
D	b	3972	GTAACGCGGTTTAATAACAGTAGCGACCCCTTGGGGTTGTTGAGCGAGTTAGT
Q	y	316	- - - - -
D	b	4032	TGCGTTGTGAGGGCTTTAGTTAAACACAGAGCCTGGCACGAGTGAATGCGTAAA
Q	y	316	- - - - -
D	b	4092	GTCCGTATTGTTCTTAAAGGTGGAACTCGGTCTCCCCACCGGCCCGGACGCC
Q	y	317	- - - - - SerL 
D	b	4152	CAGGGTCTGGGANTAGAAGACTACTAATTTTGCATGTTCTCTCTCGSGCTCCA 
Q	y	320	GlyGlyGluGluArgValLeuGluLySgluGluGluAspAspAspGluAspG
D	b	4211	GGTGAGAGAGCGAGTACTTGAGAAAGAGAGAGAGATGATGTAAGATG
Q	y	340	GluGluAspAspValSerGluGlySerGluValProGluSerAspArgProAlag
D	b	4271	GAAAGAAGATGATGTCTAGAGGCTCTGAAGTCCCGAGAGTACCCTCTCTGCG
Q	y	360	GlnHisHISglnLeuasnGlyGluArgGlyProGlnSerAlaLySgLuArgVall
D	b	4331	CAGCACCAACAGCTTAACGGCGAGCGGGACCTCAGAGTGCACAAGAGAGGGTCA
Q	y	380	TprThrProCySglyProHisGlnGlyGluAspGluGlyArgGlyProAlaProG
D	b	4391	TGGAACCCCTCGGACCGCACACAGGGCCAGGATGAAGGGCGGGGGCAGCCCCGG
Q	y	400	GlyThrArgGlnValPheSerMetAlaAlaMetAsnLySgLucIgLyThr- - - - -
D	b	4451	GGCACCCGCCAGGTGTTCTCATGCGAGCCATGAACAAGAAAGGGGGAACAGGTA 
Q	y	416	- - - - -
D	b	4511	CCCTCTGGGTGGGAGAGGTGCTAGGTGGAGAGGAACCTCAGCCCGGACAAAGC
Q	y	417	- - - - - AlaSerVallAlaThrGlyProAspSerProSerl 
D	b	4571	ACAGGTGTTTTTTTCTTCCACAGCTTCTGTGTGCCACCGGCCCAGACTCCCCGTC
Q	y	429	IproLeuProProGlyLySProAlaLeuProGlyAlaAspGlyThrProPheGly 
D	b	4631	GCCTTTGCCCCCAGCAAACACAGCCCTTACCTGGGGCGCAGGGAACCCCTTTGGC 
Q	y	449	o - - - - -
D	b	4691	GTAAGTTGGGATATTGGAGACATGGGGGTGCTCTCAGGTGTGTGTGACAGCCAGI
Q	y	450	- - - - - ProGlyArgLySgLuLy 
D	b	4751	CATCCGTGTTCACTGTGTCTGTTTGTGTTTGTGACAGTCCCCGGGCGCAAGAGAA 

AspProValGluTrpThrValMetAspValValGluTyrPheThrGluAlaGlyPheP 477  
 IGATCCCGTCGAGTGGACCGTGATGGATGCTGCGAATATTTTACTGAGGCTGATTC 4870  
 GlnAlaThrAlaPheGlnGlu----- 485  
 GAGCAGGCGACAGCTTTTCCAGA-GCAGGTGAGTTTCCAGCCGAGGACTACACACTGA 4929  
 ----- 485  
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 GlnGluLeuAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGlyL 505  
 XGAGAAATGATGTCGCAATCTTTTGTCTCATGCGAGCGCACAGATGTCTACCGGCC 5049  
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 TCCATCCCGCCTCGGGCCAGCCCTGAAATCTACGAGCACCATCAAGGTGCTTCAGC 5109  
 GlyHisPheGluAspAspProAspGlyPheLeuGly 538  
 GGCCACTTTGAGGATGATGACCCCGATGGCTTCTTAGGC 5150

plication US/10023523  
 US20020152485A1

ATION:  
 es, Ann M.

aw, Robert S.  
 rjona, Anibal A.

NTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
 NTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

NTION: ATHEROSCLEROSIS  
 E: 10797-004001

CATION NUMBER: US/10/023,523  
 3 DATE: 2001-12-17

TION NUMBER: US/09/616,289  
 DATE: 2000-07-14

TION NUMBER: US/09/517,849  
 DATE: 2000-03-02

TION NUMBER: US/08/979,608  
 DATE: 1997-11-26

TION NUMBER: US/60/031,930  
 DATE: 1996-11-27

TION NUMBER: US/60/048,547  
 DATE: 1997-06-03

ID NOS: 53  
 :SEQ for Windows Version 4.0

;  
 to sapiens

6,82e-131 Length: 12425  
 2616.50 Matches: 536  
 Y: 69.16% Conservative: 0  
 69.16% Mismatches: 2  
 91.81% Indels: 239  
 13 Gaps: 4

(1-538) x US-10-023-523-50 (1-12425)

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 GCGGGGCCCCGGCCCTACCCCGCGAGACGCGCGCGCCGACACACGCGGCC 2891

AlaSerSerAlaAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIleAsp 40

Db 2892 GCAGCCCTCGTCTCCGCGCTTCCCGCACTTACCAAGAGTGATCCTTGACAC  
 QY 41 SerLeuArgSerArgLysAlaArgProAspLeuGluArgIleCysArgMetVa  
 Db 2952 TCCTGGCTCGCCAAAGGCGCGGACCTGGAGCGCATCTCCCGGATGGT  
 QY 61 ArgHisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleG  
 Db 3012 CGGACGCGCCCGAGCGGAGCGCACCGCGCGCGAGCTCGAGAACTGATCCA  
 QY 81 AlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaA  
 Db 3072 GCGTGTCTCCGGGTACGTACAAGGGAGCATCTCGTACCGCAACGCGGCGG  
 QY 101 ProProArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyAl  
 Db 3132 CGGCGCGCGCGGAGCGCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGG  
 QY 121 AlaAlaAlaAlaAlaProProProProThrProAlaProProProProAl  
 Db 3192 GCGG  
 QY 141 AlaAlaAlaAlaProAlaArgAlaProArgAlaAlaAlaAlaAlaAlaThrAl  
 Db 3252 GCGG  
 QY 161 SerProGlyProAlaGlnProGlyProArgAlaGlnArgAlaAlaProLeuAl  
 Db 3312 TCGCTGGCGG  
 QY 181 ProProAlaProAlaAlaProProAlaAlaAlaProProAlaGlyProArgAl  
 Db 3372 CGGCGG  
 QY 201 ProProAlaValAlaAlaArgGluProProLeuProProProProGlnProPr  
 Db 3432 CGGCGG  
 QY 221 ProGlnGlnGlnProProProProGlnProGlnProGlnProProGlnGly  
 Db 3492 CCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC  
 QY 241 ArgAlaGlyGlyAlaAlaArgProValSerLeuArgGluValValArgTyrLeu  
 Db 3552 CGGCGG  
 QY 261 SerGlyGlyAlaGlyArgLeuThrArgGlyArgValGlnGlyLeuLeuGlu  
 Db 3612 AGCGG  
 QY 281 AlaAlaAlaArgGlyArgLeuGluArgThrArgLeuGlyAlaLeuAlaLeuPro  
 Db 3672 GCGCGCGCTCGAGCGCGCTCGAGCGCACCCCGCTCTCGGAGCGCTTGCCTGCC  
 QY 301 AspArgProGlyArgAlaProProAlaAlaSerAlaArgProSerArg-----  
 Db 3732 GACAGCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG  
 QY 316 -----  
 Db 3792 GCGCGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG  
 QY 316 -----  
 Db 3852 GCGAGTCCCGGAGGAACTGGTGGCGGCGGCTGGTGGGCGCTTTTGGCGCGGTTTC  
 QY 316 -----  
 Db 3912 CTCGGTGGTGGTGACCTTGGCAAGTGATTGAATCTCCCGGAGCGCTCAGTTTTC  
 QY 316 -----

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 ----- 316  
 AGTTGTCGAGGGCTTTAGTTAAACACAGAGCTGGCACGAGTGAATGCGTAAAGATTA 4091  
 ----- 316  
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 ----- SerLysArg 319  
 XGTCCTGGATTAGAACAGCTACTAATTTTGCATGCTTCTCTCTCGGCTCCAG-AGA 4210  
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 ThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThr- 416  
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 ----- 416  
 TCTGGTGGGGAAGAGTGTAGTGGAGAGGAAGTCTAGCCCGAAGACAAAGCCAAAG 4570  
 -----AlaSerValAlaThrGlyProAspSerProSerProVa 429  
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 ----- 485  
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 Db 5110 AAGCCCACTTTAGGATGATGACCCCGATGGCTTCTTAGGC 5150  
 RESULT 10  
 US-10-616-187-50  
 ; Sequence 50, Application US/10616187  
 ; Publication No. US20040013668A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lees, Ann M.  
 ; APPLICANT: Lees, Robert S.  
 ; APPLICANT: Law, Simon W.  
 ; APPLICANT: Arjona, Anibal A.  
 ; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
 ; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TRE.  
 ; TITLE OF INVENTION: ATHEROSCLEROSIS  
 ; FILE REFERENCE: 10797-004001  
 ; CURRENT APPLICATION NUMBER: US/10/616,187  
 ; CURRENT FILING DATE: 2003-07-09  
 ; PRIOR APPLICATION NUMBER: US/09/616,289  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: US 09/517,849  
 ; PRIOR FILING DATE: 2000-03-02  
 ; PRIOR APPLICATION NUMBER: US 08/979,608  
 ; PRIOR FILING DATE: 1997-11-26  
 ; PRIOR APPLICATION NUMBER: US 60/031,930  
 ; PRIOR FILING DATE: 1996-11-27  
 ; PRIOR APPLICATION NUMBER: US 60/048,547  
 ; PRIOR FILING DATE: 1997-06-03  
 ; NUMBER OF SEQ ID NOS: 53  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 50  
 ; LENGTH: 12425  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-616-187-50  
 Alignment Scores:  
 Pred. No.: 6,82e-131 Length: 12425  
 Score: 2616.50 Matches: 536  
 Percent Similarity: 69.16% Conservative: 0  
 Best Local Similarity: 69.16% Mismatches: 2  
 Query Match: 91.81% Indels: 239  
 DB: 15 Gaps: 4  
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 QY 1 MetAlaGlyProProAlaLeuProProGluThrAlaAlaAlaAlaThrThrA  
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 QY 21 AlaAlaSerSerSerAlaAlaSerProHisTyrGlnGluTrrPileLeuAspThri  
 Db 2892 GCCGCTCGTCTGTCGCGGCTTCCCGGCACCTACCAAGAGTGGATCTCGACACCA  
 QY 41 SerLeuArgSerArgLysAlaArgProAspLeuGluArgLleCysArgMetVala  
 Db 2952 TCGCTGCTCCTCGCGAAGCGCGCGGACCTGGAGCGCATCTGCGGATGCTGC  
 QY 61 ArgHisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGlnG  
 Db 3012 CGGCACGGCGCGGAGCGGAGCGGCGCGCGCGGAGCTTCGAGAAACTGATCCAGC  
 QY 81 AlaValLeuArgValSerTyrLysGlySerTyrArgAsnAlaAlaAArgVe  
 Db 3072 GCCGTGCTCCGGGTGAGCTACAGGGAGCATCTCTACCCGCAACCGCGCGCGGT  
 QY 101 ProProArgArgGlyAlaThrProProAlaProProArgAlaProArgGlyAlaPr  
 Db 3132 CCGCCCCGCGCGGAGGACCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG  
 QY 121 AlaAlaAlaAlaAlaProProProThrProAlaProProProProProProAlaPr

Db	4271	GAAGAAGATGATGTGTGACAGGGCTCTGAAGTGCCGAGAGTGACCGCTCGTGG	
QY	360	GlnHisHisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgVal	
Db	4331	CAGCACCAACAGCTTAAAGCGCGGGGACCTCAGATGGTCCAAAGAGAGGGGT	
QY	380	TrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaArg	
Db	4391	TGGACCCCTCGCGACCGCACAGCGCCAGGATGAAGGCGGGGGCCAGCCCC	
QY	400	GlyThrArgGlnValPheSerMetAlaMetAsnLysGluGlyGlyThr--	
Db	4451	GGACCCCGCAGGTGTTCTCATGGCAGCCATGAACAAGGAAGGGGAAACAGG	
QY	416	-----	
Db	4511	CCCTCTGGGTGGGAGAGTGCTAGGTGGAGAGGAACTCAGCCCGAAGACAA	
QY	417	-----AlaSerValAlaThrGlyProAspSerProS	
Db	4571	ACAGTGTTTTTTTCCCTCCAGCTTCTGTGGCCACCGCGCCAGACTCCCGCT	
QY	429	IProLeuProGlyLysProAlaLeuProGlyAlaAspGlyThrProPheG	
Db	4631	GCCTTGCCTCCAGGCAACAGCCCTACCTGGGGCGACGGACACCCCTTTGG	
QY	449	O-----	
Db	4691	GTAAGTGGGGTATTGGAGACATGGGGTGCTGCTCAGGTGTGTGTACAGCGC	
QY	450	-----ProGlyArgLysGlu	
Db	4751	CATCCGTGTTCACTGGTGCTGTGTTGTTTGAATGACAGTCCCAGGCGCAAGAGI	
QY	457	erAspProValGluTyrThrValMetAspValValGluTyrPheThrGluAlaC	
Db	4811	CTGATCCGTCGAGTGGACCGTGATGGATGTGCTGCAATATTTTACTGAGGCTC	
QY	477	roGluGlnAlaThrAlaPheGlnGlu-----	
Db	4871	CGGAGCAGCGCAGACTTCCAGA--GCAGGTGAGTTTCCAGCCCGAGACTACF	
QY	485	-----	
Db	4930	CAGACACAGAGGGCTCCCTCGGATGTGCGCTGATCCCGGCTTTCTCTGTTCCT	
QY	486	--GlnGluIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuT	
Db	4990	CCAGGAAATTGATGGCAATCTTTGCTGCTCATGACGCGACAGATGTGCTCA	
QY	505	euSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisIleLysValL	
Db	5050	TGTTCATCGCTCGGGCGAGCCCTGAAATCTACGAGCACCAATCAAGGTGC	
QY	525	InGlyHisPheGluAspAspProAspGlyPheLeuGly 538	
Db	5110	AAGGCCACTTTGAGATGATCAGCCCGATGGCTCTTTAGGC 5150	

US-09-976-740-48  
; Sequence 48, Application US/09976740  
; Publication No. US20020194633A1  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; APPLICANT: Arjona, Anibal A.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREA  
; TITLE OF INVENTION: ATHEROSCLEROSIS  
; FILE REFERENCE: 10797-004001  
; CURRENT APPLICATION NUMBER: US/09/976,740  
; CURRENT FILING DATE: 2001-10-12

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|CGGCCCCCGC CGCGCGCGCGCGCGCGCGCGCGGGAGTCGC GCGTGC GC CGCGCGCG 899

ees, Ann M.  
 Lees, Robert S.  
 Law, Simon W.  
 Arjona, Anibal A.  
 ENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
 ENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
 ENTION: ATHEROSCLEROSIS  
 CE: 10797-004001  
 ICATION NUMBER: US/10/671,242  
 NG DATE: 2003-09-24  
 ATION NUMBER: US/09/616,289  
 DATE: 2000-07-14  
 ATION NUMBER: US 09/517,849  
 DATE: 2000-03-02  
 ATION NUMBER: US 08/979,608  
 DATE: 1997-11-26  
 ATION NUMBER: US 60/031,930  
 DATE: 1996-11-27  
 ATION NUMBER: US 60/048,547  
 DATE: 1997-06-03  
 ID NOS: 53  
 tSEQ for Windows Version 4.0

## Yctolagus cuniculus

S  
 46)....(1895)

: 3.48e-130 Length: 2561  
 2594.00 Matches: 503  
 ty: 94.20% Conservative: 17  
 arity: 91.12% Mismatches: 16  
 91.02% Indels: 16  
 12 Gaps: 8

(1-538) x US-10-671-242-48 (1-2561)

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 XCCGCTCGTCTCCGCGCTTCCCGCACTACCAAGAGTGGATTCTGCACACCATC 365  
 SerLeuArgSerArgLysAlaArgProAspLeuGluArgLysCysArgMetValArg 59  
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 ArgHisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGlnGln 79  
 CGGACGCGCGCGAGCGGAGCGGACGCGCGCGCGCTCGAGAACTGATCCAGAG 485  
 AlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAlaArgVal 99  
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 ProProArgArgGlyAlaThrProProAlaProProAlaProProArgGlyAlaPro 119  
 CCGCGCGCGGAGCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 605  
 AlaAlaAlaAlaAlaProProProProAlaProProAlaProProProProAlaPro 139  
 ---GCCCG 659  
 ---AlaAlaAlaAlaProAlaArgAlaProArg-----AlaAlaAlaAlaAla 156  
 3CG 719

QY 157 ThrAlaProProSerProGlyProAlaGlnProGlyProArgAlaGlnArgA  
 Db 720 ACAGCGCCCTCGCCCGCCCGCGCGAGCGCGCGCGCGCGCGCGCGCGCG  
 QY 177 LeuAlaAlaProProAlaProAlaProAlaProAlaValAlaProAla  
 Db 780 CTGCG  
 QY 197 ArgArgAlaProProPro-----AlaValAlaAlaArgGluProProLeuPr  
 Db 840 CG  
 QY 215 ProGlnProProAlaProProGlnGlnGln-----ProPr  
 Db 900 CCACAGCG  
 QY 230 GlnProGlnProProGluGlyGlyValAlaValArgAlaGlyGlyAlaAlaA  
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 QY 310 AlaSerAlaArgProSerArgSerLysArgGlyGlyGluGluArgValLeuGly  
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 Db 1260 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
 QY 348 SerGluValProGluSerAspArgProAlaGlyAlaGlnHisGlnLeuAsn  
 Db 1320 TGGAGGTGCGCGAGCGATCGTCCCGCGGTGCGCGAGCATCACAGCTGAT  
 QY 367 GluArgGlyProGlnSerAlaLysGluArgValLysGluThrThrProCysGly  
 Db 1380 GAGCGCGCGCGCGAGCCCAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG  
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 Db 1440 CCTGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
 QY 407 MetAlaAlaMetAsnLysGlyGlyGlyThrAlaSerValAlaThrGlyProAsp  
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 Db 1560 TCCCGGTGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG  
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 Db 1680 GTGCTGAGTACTTACCGAGCGCGCTTCCCTGAGCAAGCACCGCTTTCAGG  
 QY 487 GluIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspValLeuThrGlyL  
 Db 1740 GAGATCGAGCGGAGTCCCTGCTCATGACGCGCACGATGCTCTCACCGCGC  
 QY 507 IleArgLeuGlyProAlaLeuLysIleTyrGluHisHisIleLysValLeuGlnG

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CGCCTGGGGCCAGCGCTTGAATAATATAGACCAATATCAAGGTCTGTCAGCAGGT 1859

sPhcGluAspAspAspProAspGlyPheLeuGly 538
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pplication US/10023529
US20020129388A1
TION:
s, Ann M.
es, Robert S.
w, Simon W.
Joná, Anibal A.
TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TION: ATHEROSCLEROSIS
3: 10797-004001
ATION NUMBER: US/10/023,529
DATE: 2001-12-17
TION NUMBER: 09/616,289
DATE: 2000-07-14
TION NUMBER: US 09/517,849
DATE: 2000-03-02
TION NUMBER: US 08/979,608
DATE: 1997-11-26
TION NUMBER: US 60/031,930
DATE: 1996-11-27
TION NUMBER: US 60/048,547
DATE: 1997-06-03
ID NOS: 53
SEQ for Windows Version 4.0

ctolagus cuniculus

6) ... (1895)

3 48e-130 Length: 2561
2594.00 Matches: 503
Y: 94.20% Conservative: 17
ity: 91.12% Mismatches: 16
91.02% Indels: 16
13 Gaps: 8

(1-538) x US-10-023-529-48 (1-2561)

AlaGlyProProAlaLeuProProGluThrAlaAlaAlaThrThr---Ala 19
CGCGGGCCCCCGGCCCTACCCCGCGGAGACGGCGCGCGCCACACCGCGCG 305
AlaAlaSerSerSerAlaAlaSerProHisTyrGlnGluTrpIleLeuAspThrIle 39
CGCGCTCGTGTCTGCGCGCTTCCCGGCATACCAAGAGTGGATTCTGCAACCATC 365
SerLeuArgSerArgLysAlaArgProAspLeuGluArgLysCysArgMetValArg 59
TCGTGCGCTCGCGCAAGCGCGCGGACCTGGAGCGCATCTGCCGATGTGCGG 425
ArgHisGlyProGluProGluArgThrArgAlaGluLeuGluLysLeuIleGlnGln 79
GGCACGGCCCGGAGCGGAGCGCACGCGCGCGAGCTCGAGAACTCATCCACGAG 485
AlaValLeuArgValSerTyrIlysclySerIleSerTyrArgAsnAlaAlaArgVal 99
CGCGTCTCGGGTCACTACAGGGGAGCATCTGTACCGCAACGCGGCGCGCTC 545

```

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|||||
|CTGCCCTGCGCGCGCAAGAGAGCGCGAGACCCCGTGGAGTGACAGTATGAC 1679
|ValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGluGln 486
|CTGGAGTACTTCCAGGCGCGCTTCCCTGAGCAAGCCACGGCTTCCAGGAGCAG 1739
|uileAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSer 506
|GATCAGCGCAAGTCCCTGCTCTATGAGCGCGACCGATGCTCTCACGGCTGTC 1799
|eArgLeuGlyProAlaLeuLysIleTyrGluHisIleLysValLeuGlnGlnGly 526
|CCGCTGGCGCGCAGGTTGAAATCTATGAGCACCATATCAAGGTGCTGCACAGG 1859
|sPheGluAspAspAspProAspGlyPheLeuGly 538
|CTTGAGGACGATGACCGGAGGCTTCTCGGA 1895

```

```

pplication US/10023523
: US20020152485A1
ATION:
es, Ann M.
aw, Simon W.
zjona, Anibal A.
TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TION: ATHEROSCLEROSIS
E: 10797-004001
CATION NUMBER: US/10/023,523
3 DATE: 2001-12-17
TION NUMBER: US/09/616,289
DATE: 2000-07-14
TION NUMBER: US 09/517,849
DATE: 2000-03-02
TION NUMBER: US 08/979,608
DATE: 1997-11-26
TION NUMBER: US 60/031,930
DATE: 1996-11-27
TION NUMBER: US 60/048,547
DATE: 1997-06-03
ID NOS: 53
:SEQ for Windows Version 4.0

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/ctolagus cuniculus

{6}...(1895)

```

3 48e-130 Length: 2561
2594.00 Matches: 503
y: 94.20% Conservative: 17
rity: 91.12% Mismatches: 16
Indels: 16
13 Gaps: 8

```

(1-538) x US-10-023-523-48 (1-2561)

```

AlaGlyProAlaLeuProProGluThrAlaAlaAlaThrThr---Ala 19
|GCGGGCCCCCGGCTTACCCCGGAGAGCGCGCGCGCGCGCGCGCGCGCG 305

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```

AlaLaserSerAlaLaserProHisTyrGlnGluThrIleLeuAspThrIle 39
|GCCGCTCGTCTGCGCGCTTCCCGCACTACCAAGAGTGTGATTTCTGGACCATC 365

```

```

Qy 40 AspSerLeuArgSerArgLysAlaArgProAspLeuGluArgLysCysArgMe
Db 366 GACTCGCTGCGCTCGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 60 ArgArgHisGlyProGluProGluArgThrArgAlaGluLeuGlyLysLeuI
Db 426 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 80 ArgAlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaA
Db 486 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 100 GlnProProArgArgGlyAlaThrProProAlaProProArgAlaProArgG
Db 546 CAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 120 AlaAlaAlaAlaAlaAlaProProProThrProAlaProProProProPr
Db 606 -----GCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 140 Val---AlaAlaAlaAlaProAlaArgAlaProArg-----AlaAlaAla
Db 660 GTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 157 ThrAlaProProSerProGlyProAlaGlnProGlyProArgAlaGlnArgAl
Db 720 ACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 177 LeuAlaAlaProProProAlaProAlaProAlaProAlaValAlaProAla
Db 780 CTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 197 ArgArgAlaProProPro-----AlaValAlaAlaArgGluProProLeuPr
Db 840 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 215 ProGlnProProAlaProProGlnGlnGln-----ProPr
Db 900 CCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 230 GlnProGlnProProProGluGlyGlyAlaValAlaGlyGlyAlaAlaArg
Db 960 CAGCCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 250 SerLeuArgGluValValArgTyrLeuGlyGlySerGlyGlyAlaGlyGlyArg
Db 1020 AGCTTCGGGAGAGTCTGCTGCTTACCTCGGGGGGTAGCAGCGCGCTGGCGCG
Qy 270 ArgGlyArgValGlnGlyLeuLeuGluAlaAlaAlaAlaArgGlyArgLeu
Db 1080 CGCGCGCGCGTGCAGGGTCTGCTGGAGAGAGGCGCGCGCGCGCGCGCGCTG
Qy 290 ThrArgLeuGlyAlaLeuAlaLeuProArgGlyAspArgProGlyArgAlaPro
Db 1140 ACCCGTCTCGAGCGCTTTCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 310 AlaSerAlaArgProSerArgSerLysArgGlyGlyGluGluArgValLeuGlu
Db 1200 GCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 330 GluGluGluAspAspGluAspGluAspGluGluAspGluAsp-----ValSer
Db 1260 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
Qy 348 SerGluValProGluSerAspArgProAlaGlyAlaGlnHisGlnLeuAsn-
Db 1320 TCGAGGTGCGCGAGAGCGATCGTCCCGCGCGCGCGCGCGCGCGCGCGCG
Qy 367 GluArgGlyProGlnSerAlaLysGluArgValLysGluThrThrProCysGly
Db 1380 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
Qy 387 GlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThrArgGlnVal

```

GCACGAGGAAGCGGGGCCCGCCGGGAGTGGCACCCCGCAGGTGTCTCTCC 1499

AlalaMetAanLysGluGlyThrAlaSerValAlaThrGlyProAspSerPro 426

GCAGCCTTGACTAAGAGGGGGGATCAGCCTTCGACCACCGGGCCTGACTCCCCG 1559

ProValProLeuProGlyLysProAlaLeuProGlyAlaAspGlyThrProPhe 446

CCGCTGCTTTGGCCCCCGGAAGCCAGCCCTCCCGAGGCGCATGGACCCCCTTT 1619

CysProGlyArgLysGluLysProSerAspProValGluTrpThrValMetAsp 466

TGCCCTGCCGGCGCAAAAGAAGAACCCGGCAGACCCCGTGGAGTGGACGTCATGGAC 1679

ValGluTrpPheThrGluAlaGlyPheProGluGlnAlaThrAlaPheGlnGluGln 486

GTCGAGTACATTACCGAGGGCGGGCTTCCTCTAGCAAGCCACGGCTTTCAGGAGCAG 1739

IleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSer 506

ATCGACGGCAAGTCCTCTGCTCATGCGGCGCACCGATGCTCTCACCGGCCCTGTCTCC 1799

ArgLeuclyProAlaLeuLysIleTyrgluHisIleLysValLeuGlnGlnGly 526

CGCTGGGGCGCAGCGTTGAAAATCTATGAGCACCATATCAAGGTGCTGCAGCAGGGT 1859

PheGluAspAspAspProAspGlyPheLeuGly 538

TTGAGGACCATGACCGCGAAGGCTTCTCTGGGA 1895

publication US/10616187  
US20040013668A1  
TION:  
s, Ann M.  
es, Robert S.  
ona, Anibal A.  
w, Simon W. A.  
TION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TION: ATHEROSCLEROSIS  
: 10797-004001  
ATION NUMBER: US/10/616,187  
DATE: 2003-07-09  
ION NUMBER: US/09/616,289  
ATE: 2000-07-14  
ION NUMBER: US 09/517,849  
ATE: 2000-03-02  
ION NUMBER: US 08/979,608  
ATE: 1997-11-26  
ION NUMBER: US 60/031,930  
ATE: 1996-11-27  
ION NUMBER: US 60/048,547  
ATE: 1997-06-03  
ID NOS: 53  
SEQ for Windows Version 4.0

ctolagus cuniculus

6) ... (1895)

3.48e-130	Length:	2561
2594.00	Matches:	503
94.20%	Conservative:	17
91.12%	Mismatches:	16
91.02%	Indels:	16

DB:	15	Gaps:	8
US-09-376-740-43 (1-538) x US-10-616-187-48 (1-2561)			
QY	1	MetaAlaGlyProProAlaLeuProProGluThrAlaAlaAlaAlaAlaAlaThrThr	
Db	246	ATGGCGGGGCCCCCGCCCTACCCCGCGGAGACGGCGCGCGCCACACGCG	
QY	20	AlaAlaAlaSerSerAlaAlaSerProHisTyrGlnGluTupileLeuAsp	
Db	306	GCGCGCGCTCTGCTCGCGCGCTTCCCGCACATACCAGAGTGGATCTTGGAC	
QY	40	AspSerLeuArgSerArgLyAlaArgProAspLeuGluArgIleCysArgMet	
Db	366	GACTCGCTGCTGCGCAGCGCGCGCGACCTCGAGCGCATCTGCGCGATG	
QY	60	ArgArgHisGlyProGluProGluArgThrArgAlaGluLeuGluIysLeuIle	
Db	426	CGCGCGGACGGCCGAGCCGAGCGCACGCGCGCGCGAGCTCGAGAAACTGATC	
QY	80	ArgAlaValLeuArgValSerTyrLysGlySerIleSerTyrArgAsnAlaAla	
Db	486	CGCGCGGTGCTCGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACCGCGCG	
QY	100	GlnProProArgArgGlyAlaThrProProAlaProProArgAlaProArgGly	
Db	546	CAGCGCGCGCGCGAGGCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGG	
QY	120	AlaAlaAlaAlaAlaAlaProProProThrProAlaProProProProPro	
Db	606	-----GCCGCGCGCGCGCGCGCGCGCCACCGCGCGCGCGCGCGCGCGCG	
QY	140	Val---AlaAlaAlaAlaProAlaArgAlaProArg-----AlaAlaAlaAla	
Db	660	GTGCGTC	
QY	157	ThrAlaProProSerProGlyProAlaGlnProGlyProArgAlaGlnArgAla	
Db	720	ACAGCGG	
QY	177	LeuAlaAlaProProAlaProAlaAlaProProAlaValAlaAlaProAlaG	
Db	780	CTGGCGG	
QY	197	ArgArgAlaProProPro-----AlaValAlaAlaArgGluProProLeuPro	
Db	840	CGG	
QY	215	ProGlnProProAlaProProGlnGlnGlnGln-----ProProPro	
Db	900	CCACAGCG	
QY	230	GlnProGlnProProProGluGlyGlyAlaValArgAlaGlyGlyAlaAlaArgP	
Db	960	CAGCCACAGCGCGCGCGAGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	
QY	250	SerLeuArgGluValValArgTyrLeuGlyGlySerGlyGlyAlaGlyGlyArgL	
Db	1020	AGCTTGGGGGAGTCTGCTGCTACTCTGGGGGTAGCAGCGCGCGCTGGCGCGCG	
QY	270	ArgGlyArgValGlnGlyLeuLeuGluGluAlaAlaAlaArgGlyArgLeuG	
Db	1080	CGCGCGCGCTGCGAGGGTCTGCTGGAAGAGGAGCGCGCGCGCGCGCGCGCTGG	
QY	290	ThrArgLeuGlyAlaLeuAlaLeuProArgGlyAspArgProGlyArgAlaProP	
Db	1140	ACCCGCTCTCGAGCGCTTGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCAC	
QY	310	AlaSerAlaArgProSerArgSerLysArgGlyGlyGluGluArgValLeuGluL	
Db	1200	CCACAGCGCGCGCGCGGAGAACAGAGAGCTGGCGGAGCGAGCTGCTTGAA	
QY	330	GluGluAlaAspAspGluAspGluAspGluAlaAspGluAlaAsp-----ValSerG	

us-09-976-740-43.rnpb

: March 13, 2004, 04:27:21  
55 sec